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; LENGTH: 2494
; TYPE: DNA
; ORGANISM: Homo s
US-09-649-163-9696
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LENGTH: 2494
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Best Local Similarity
Matches 1564; Conserv
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CURRENT APPLICATION NUMBER: US/09/652,12)
CCURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,132
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEO ID NOS: 10051
SOFTWARE: FASTSEQ for Windows Version 4
SEQ ID NO 10026
LENGTH: 2494
TYPE: DNA
ORGANISM: Homo sapiens
US-09-652-126-10026
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                                                                                                                                                                                                                                             Sequence 10026, Application US/09652126 GENERAL INFORMATION:
                                 Query Match
Best Local Similarity
                       Matches
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1 GCCCCACAGCCGGCCTGCGACGCCCGGCTGGGCAGCAGCCGATAAGGAGCTGAAGGCAGG 60

Conservative

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; TYPE: DNA; ORGANISM: Homo sapiens US-09-652-913-10528 Sequence 10528, Application US/09652913
GENERAL INFORMATION:
APPLICATIC FAIL, Dean R.
TITLE OF INVENTION: NOVEL NUCLEIC ACID TITLE OF INVENTION: "HEREFOR FILE REFERENCE: 1600.1174-001
CURRENT APPLICATION NUMBER: US/09/652.9 TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1174-001
CURRENT FILING DATE: 2000-08-31
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,107
PRIOR APPLICATION NUMBER: 60/152,107
PRIOR FILING DATE: 1093-08-31
NUMBER OF SEQ ID NOS: 10833
SOFTMARE: FastsEQ for Windows Version 4.0
LENGTH: 2494 Query Match Best Local : Match 98.5%; Local Similarity 99.5%; Score 1548.8; Pred. No. 2.9 .9e-298; .es 7; Indels 1; Gaps DB 25; Length 2494;

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Sequence 8605, Application US/09652918
GENERAL INFORMATION:
GALVIN, Katherine
APPLICANT: GALVIN, Katherine
APPLICANT: HOLTZMAN, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID I
TITLE OF INVENTION: THEREPORE
FILE REFERENCE: 1600.1187-001
CURRENT APPLICATION NUMBER: US/09/652,91:
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,130
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEO ID NOS: 8985
SOFTMARE: FASTSEQ for Windows Version 4
SEO ID NO 8805
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TYPE: DNA
ORGANISM: Homo
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US-09-663-784-702
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GENERAL INFORMATION:
APPLICANT: GALVIN, Katherine
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: 1600.1160-001
CURRENT APPLICATION NUMBER: US/09/663,784
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 60/154,571
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 830
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 98.5%; Score 1548.8; DB 26; Length 2494;
Best Local Similarity 99.5%; Pred. No. 2.9e-298;
Matches 1564; Conservative 0; Mismatches 7; Indels 1; (
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                                                                                    AGCTTCCTTGAACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAA
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US-09-699-998-8671; Sequence 8671, A GENERAL INFORMAT

Sequence 8671, Appli GENERAL INFORMATION:

Application

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LENGTH: 2494
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Holtzman, Douglas APPLICANT: Gearing, David P. TITLE OF INVENTION: NOVEL NUC TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.2008-001
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                                     GGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTT
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          CCTGCGTCTGGCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAG
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RESULT 14

US-09-710-286-2850

Sequence 2850, Application US/09710286

GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: McCarthy, Sean A.
APPLICANT: HOLTZMAN, DOUGLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION UNMBER: US/09/710,286
CURRENT FILLING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 60/164,255
PRIOR FILLING DATE: 1999-11-09
NUMBER OF SEG ID NOS: 4115
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                           CCTTGTGCCACTGGAGGAGCCAGTGCCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTT 899
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GGACCTAGACAGTCAGAAGTATCGGCCTCTGGGGAGATGCGCTTCACTCTGGGCACCTT 1601
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RESULT 15
US-09-716-953-1866
Sequence 1866, Application US/09716953; GENERAL INFORMATION:
                                                                                                                  SOFTWARE: Fas
SEQ ID NO 1866
LENGTH: 2494
                          Query Match
Best Local Similarity
Matches 1564; Conserv
                                                                            TYPE: DNA
ORGANISM: Homo
-09-716-953-1866
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/716,953
CURRENT FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/167,413
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 2620
                                                                                                                                                                                                                 APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: McCarthy, Sean
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES
TITLE OF INVENTION: THERREFOR
FILE REFERENCE: 1600.2044-001
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                                                    CATGCTGCTGCGCCTCTTCCTGGCCATGGAGAAGGCCAGGCATATGGAGTATGAATGCCC
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Search completed: May 17, 2003, 15:40:37 Job time: 3804 secs

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 40620, A Sequence 139382, Sequence 1811, Ap Sequence 1797, Ap Sequence 1812, Ap Sequence 138510, Sequence 138513, Sequence 138514,	Sequence 1781, Ap Sequence 5904, Ap Sequence 5904, Ap Sequence 22, Appl Sequence 12897, A Sequence 1582, A Sequence 429, App Sequence 2505, Ap Sequence 2517, Ap	Sequence 1155, Ap Sequence 25, Appl Sequence 25, Appl Sequence 3940, Ap Sequence 1180, Ap	Description

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ALIGNMENTS

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APPLICANY: Williamson, Mark
TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 2247, 2167, 2935,
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TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
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TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 16344, 8941, 9911, 27444, 50566 OR 66428 MOLECULE
TITLE OF INVENTION: 1000 BEER: US 60/353,600
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/371,075
PRIOR APPLICATION NUMBER: US 60/371,075
PRIOR APPLICATION NUMBER: US 60/371,194
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR APPLICATION NUMBER: US 60/378,035
PRIOR APPLICATION NUMBER: US 60/378,035
PRIOR APPLICATION NUMBER: US 60/385,023
PRIOR APPLICATION NUMBER: US 60/386,853
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR APPLICATION NU
; NAME/KEY: CDS
; LOCATION: (359)...(1513)
PCT-US03-02588-25
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                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 1799
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APPLICANT: Hunter, John Joseph
APPLICANT: MacHeth, Kyle J.
APPLICANT: Tsai, Fong-Ying
APPLICANT: Lesoon, Andrea
APPLICANT: Lesoon, Andrea
                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 122
                                                                                                                             ORGANISM: Homo sapiens
                                                                                            FEATURE:
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1562; Conservative
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Sequence 25, Application US/10354358

Sequence 25, Application US/10354358

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc

APPLICANT: Hunter, John Joseph

APPLICANT: Hunter, John Joseph

APPLICANT: Hunter, John Joseph

APPLICANT: Hunter, John Joseph

APPLICANT: Lescon, Andrea

APPLICANT: Lightcap, Eric S.

APPLICANT: Lightcap, Eric S.

APPLICANT: Lightcap, Eric S.

APPLICANT: Milliamson, Mark

APPLICANT: Rudolph-Owen, Laura A.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,

TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,

TITLE OF INVENTION: 8925, 9389, 1642, 85369, 10297, 1584, 9525, 14124, 4469,

TITLE OF INVENTION: 16334, 68862, 9011, 14,031, 6178, 21225, 1420, 32236, 2094,

TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULE

FILE REFERENCE: MPIOZ-020PIRMOMNIM

THEOREM: ADDITORNIADED: HEIGHD/S4 158
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RRENT APPLICATION NUMBER: US/10/354,358
RRENT FILING DATE: 2003-01-30
IOR APPLICATION NUMBER: US 60/353,600
IOR APPLICATION NUMBER: US 60/364,517
IOR APPLICATION NUMBER: US 60/364,517
IOR FILING DATE: 2002-03-15
IOR APPLICATION NUMBER: US 60/371,075
IOR FILING DATE: 2002-04-09
IOR APPLICATION NUMBER: US 60/371,507
IOR FILING DATE: 2002-04-09
IOR APPLICATION NUMBER: US 60/371,507
IOR FILING DATE: 2002-04-10
IOR APPLICATION NUMBER: US 60/372,984
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; LOCATION: (359)...(1513)
US-10-354-358-25
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PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR APPLICATION NUMBER: US 60/382,995
PRIOR APPLICATION NUMBER: US 60/382,995
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/385,023
PRIOR HILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/388,853
PRIOR RILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR PILING DATE: 2002-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 25
LENGTH: 1799
TYPE: DNA
ORGANISM: Homo Sapiens
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                   GGACCTAGAGAGTGAGAAGTATCGGCGGTCTGGGGGAGATGCGCCTTCACTCTGGGCACCTT
                                                    GCTTCGGGGCTCCCCCCTCTCTCTCTCTCAGCCTGGGCCTGGGGCTTCATTGCTGATGT
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GGCTTCGGGGCCTGCTCTTCTCTGTGCTCAGCCTGGGCCTGGGGCTTCATTGCTGATGT
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                                                        AAAAAAAAAA 1799
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Sequence 3940, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

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PRIOR APPLICATION NUMBER: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4./
SEQ ID NO 3940
LENGTH: 1764
TYPE: DNA
ORGANISM: Human
US-09-949-016-3940
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GGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTT
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                                                           CCTGCGTCTGGCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCCTCTGTAGGAAG
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Pred. No. .8e-312;
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RESULT 5

US-10-264-237-1180/c

Sequence 1180, Application US/10264237

Sequence 1180, Application US/10264237

Sequence 1180, Application US/10264237

Sequence 1180, Application US/10264237

FILE REFERENCE: PAI31P1

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: Patentin Ver. 3.1

SEQ ID NO 1180

LENGTH: 1562

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY misc_feature
LOCATION: (7)..(7)

COTHER INFORMATION: n equals a,t,g, or c

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TCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCCTACTTGGTATATGTGC
         TCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCCTACTTGGTATATGTGC 1096
                                                       GCGTCATGCATCTGTTCTACGTGCGGGCGGGGAGTGTCTCGTGCCATGCTGCTGCGCGCCTCT 1036
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                                           GCGTCATGCATCTGTTCTACGTGCGGGCGGGAGTGTCTCGTGCCATGCTGCTGCCGCCTCT
                                                                                       FGCTGCACTCGCACCTGGGCAGTGAGATGTTTTGCTGCACCCATGGGCCGCTGTGCAGCTG 616
                                                                                                    TGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTGTGCAGCTG 976
                                                                                                                                    AGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGACGACGTTTGTGCTAGTCCTGGCAC 916
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US-10-170-235-1781

US-10-170-235-1781, Application US/10170235

Sequence 1781, Application US/10170235

SEQUENCE INFORMATION:

APPLICANT: VENTER, J. Craig

TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF

FILE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF

FILE REFERENCE: CL001380

CURRENT APPLICATION NUMBER: US/10/170,235

CURRENT FILING DATE: 2003-03-17

SEQ 1D NO 1781

SEQ 1D NO 1781

LENGTH: 1806

TYPE: NAS
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Matches 1528; Conserv
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                                             387 AGCAGGGGGGCCCCCGGGGGTAGCTCCCGGGGCCCTTGCCTATG-AGTGACTGCTGAACC 445
                                                                 120 GGTCGAGGTTATGGATCCAG----- 139
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95.4%; Pred. No. 1e-301;
tive 0; Mismatches 25; Indels 49; Gaps
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                                             GCGGTTGCGTGGAGCCCCCCCCCCCCCAGCTGGAAGCCCCCAGCAGCACCCCCCAGAAGAGC
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APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
FITLE OF INVENTION: GENETIC POLYMORPHISMS AS
FITLE OF INVENTION: MYOCARDIAL INFARCTION,
FILE REFERENCE: CL001456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILLING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5904
LENGTH: 1806
TYPE: DNA
ORGANISM: Homo sapiens
US-60-453-135-5904
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Best Local Similarity
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Matches 1523;
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CTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCGCGAGACT
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  ACCCCACGAACCAAATCCAAATAAAGTGACATTCCCAGCCTG 1558
                                            AGCCCAGCTGGGCCCAGCTGCCTATGTAAGGCCTTCTAGTTTGTTCTGAGACCCCC
                                                                                        AGCCCAGCTGGCCTGGCCCAGCTGCCTATGTAAGGCCTTCTAGTTTGTTCTGAGACCCCC 1516
                                                                                                                                       GGGTGAGAAGGTGGAGGCTATGCTTTGGGGGGACAGGCCAGAATGAAGTCCTGGGTCAGG
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001457
CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOCTWARE: POSTAGE
SEQ ID NOS: 82762
SEQ ID NO 5904
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; TYPE: DNA
; ORGANISM: HOMO Sapiens
US-60-453-050-5904
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Best Local Similarity 95.1%; Pred. No. 2.8e-301;
Matches 1523; Conservative 5; Mismatches 25;
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                                                                 {\tt ATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTATTGCTGT}
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RESULT 9
US-10-348-052-22
Sequence 22, Application US/10348052
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
APPLICANT: FYEST, Henrik
TITLE OF INVENTION: COMPOSITIONS AND METITLE OF INVENTION: OF SPHINGOLIPID METITLE OF INVENTION: OF SPHINGOLIPID METITLE REFERENCE: 200116.405
CURRENT APPLICATION NUMBER: US/10/348,0
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                     METHODS FOR METABOLISM #
                     R THE MODULATION AND/OR SIGNALING
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; CURRENT FILING DATE:
; NUMBER OF SEQ ID NOS:
; SOFTWARE: FastSEQ for
; SEQ ID NO 22
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Homo sapies
US-10-348-052-22
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Best Local Similarity
Matches 1151; Conser
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                           CTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGTC
                                                              CTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGTC
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Pred. No. 1.1e-243;
0; Mismatches 1;
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Sequence 12897, Application US/09949016

Sequence 12897, Application US/09949016

GENERAL IMPORTANIAN:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/247,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 500/231,498

PRIOR APPLICATION NUMBER: 500/231,498

PRIOR FILING DATE: 2000-09-08

SEQ ID NO 12897

LENGTH: 7195

TYPE: NAM:
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; ORGANISM: Human
US-09-949-016-12897
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Best Local :
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      CCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACCTTGTGCCACTGGAGGAGCCAG · 4 4 9 9
                              CCCCCGTTGTGGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCCACTGGAGGAGCCAG 862
                                                                                                                                        CCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTCCAAGACACCTGCCT 802
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                                                                                                       CCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTCCAAGACACCTGCCT 4439
                                                                                                                                                                                                              GGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTGGCAGCCCTGCGCA 4379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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US-09-949-016-15682

Sequence 15682, Application US/09949016

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: BOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 600-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15682
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                                                                        NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 15682
LENGTH: 7198
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                GAAGGTGGAGGCTATGCTTTGGGGGGGACAGGCCAGAATGAAGTCCTGGGTCAGGAGCCCA
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US-09-948-128-429/c

US-09-948-128-429/c

Sequence 429, Application US/09948128

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig

TITLE OF INVENTION: COLLECTION OF SINGLE NUCLECTIOE POLYMORPHISM (SNPs) LOCATED TITLE OF INVENTION: 17, METHODS OF DETECTION, AND USES THEREOF

FILE REFERENCE: CL001294

CURRENT APPLICATION NUMBER: US/09/948,128

CURRENT FILING DATE: 2001-09-07

NUMBER OF SEQ ID NOS: 465
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ORGANISM: HUMAN
FEATURE:
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                                                  CCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTATATGTGCCCGTGG
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Pred. No. 6.1e-222;
0; Mismatches 0;
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RESULT 13
US-10-144-771-2596
; Sequence 2596, Application US/10144771
; GENERAL INFORMATION:
; APPLICATT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
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: TYPE: DNA

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US-10-144-771-2596
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4624267 GCTGCAGGGCCTGTCCACAGCTCCTGTGGGGGTGGAGGAGACTCCTCTGGAGAAGGGTGA 4624208
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Pred. No. 8.6e-179;
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                                GTGGTGGGGACCCCTGCAGAGAAAGCT-AGAAGGTGGGGCTATGACTTGGAAAGAAAGGC 1800
                                                                  GTGGAGGAGACTCCTCTGGAGAAGGGTGAGAAGGTGGAGGCTATGCTTTGGGGGGGACAGG 1433
                                                                                                  GGGACCCTCCCCGCACCCACCTCCTGGTATGGGAGGTTATTTCTAAAGTTCCTATGGAA 1741
                                                                                                                                    ACTTGCAGGACCCTTCCCTTCCCTAGGGCTGCAGGGCCTGTCCACAGCTCCTGTGGGG
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APPLICANT: ELASHOFF, Michael
APPLICANT: ELASHOFF, Michael
FILE REFERENCE: 44921-509-01-US
CURRENT APPLICATION UNBER: US/10/338,044
CURRENT APPLICATION UNBER: US/10/338,044
CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 2696
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2517
LENGTH: 2648
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US-10-338-044-2517
Sequence 2517, Application US/10338044
GENERAL INFORMATION:
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Best Local Similarity
Matches 1084; Conserv
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75.3%;
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Pred. No. 7.7e-172;
0; Mismatches 342;
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US-09-949-016-40620

Sequence 40620, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307

CURRENT EPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

SEQ ID NO 40620

LENGTH: 601

TYPE: DIA

ORGANISM: Human

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Best Local Similarity 99.8%;
Matches 600; Conservative :
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                                                                                                                                                                          1272 AGAGCCCTTATGACCCCTGGGCCGCCTGTGCCTTAGTGTCTACTTGCAGGACCCTTCCT 1331
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                                                                                                                                                     AGAGCCCTTATGACCCCTGGGCCGCGCTGTGCCTTAGTGTCTACTTGCAGGACCCTTCCT 540
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Search completed: May 17, 2003, 17:00:34

Job time : 4837 secs

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AGTGGGTTCCAAGACACCTGCCTCCCCCCTTGTGGTCCAGGAGGGCCCGGTAGATGCACA
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Pred. No. 2.9e
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                                                                                                                                                            INFORMATION
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                  Pan,
                                Silos-Santiago,
                                             MacBeth, Kyle J.
Fraser, Christopher C.
Villeval, Jean-Luc M.G.
Goodearl, Andrew D.J.
         Busfield, Samantha
                            White, David
                                                                                   Richardson, Jennifer
                                                                                          Williamson, Mark
                                                                                                     McCarthy, Sean
                                                                                                               Weich,
                                                                                                                        Kingsbury,
                                                                                                                                        Galvin,
                                                                                                                      Leiby, Kevin R.
Kingsbury, Gillian
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APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLI
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1164-001
CURRENT APPLICATION NUMBER: US/09/649.163
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 60/150,608
PRIOR FILING DATE: 1999-08-25

MOLECULES

AND USES

APPLICANT:

Deeds, James Lee, John

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PRIOR FILING DATE: ,1999-07-14

NUMBER OF SEQ ID NOS: 2240

SOFTWARE: FastSEQ for Windows Version SEQ ID NO 2136
LENGTH: 2494
TYPE: DNA
ORGANISM: Homo sapiens
US-09-617-081-2136
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                                CCTTGTGCCACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGACTT 899
                                                                                      AGTGGGTTCCAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACA 839
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                                                                   AGTGGGTTCCAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACA 172:
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2442 CACAAACATGAA 2453
                        1560 AAAAAAAAAAA 1571
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                                                                                                    TGAAGTCCTGGGTCAGGAGCCCAGCTGGCTGGGCCCAGCTGCCTATGTAAGGCCTTCTAG
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RESULT 7
US-09-637-886-9797
US-09-637-886-9797, Application US/09637886

GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
APPLICANT: Gearthy, Sean A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Lloyd, Clare M.
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Jennifer
APPLICANT: Holter, John J.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1151-001
CURRENT PILNG AATE: 2000-08-09
CURRENT FILNG AATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,938
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 10397
SEO ID NO 9797
LENGTH: 2494
TYPE: DNA

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PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1783
TYPE: DNA
ORGANISM: Homo sapiens
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PCT-US02-24623-1
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APPLICANT: EXELIXIS,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SPHKS FILE REFERENCE: EX02-104
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                                              GCCTTCGGGGCTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGT
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 GGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCCTTCACTCTGGGCACCTT
            GGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTT
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Pred. No. 1.1e-298;
0; Mismatches 7;
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RESULT 6
US-09-617-081-2136
US-09-617-081-2136, Application US/09617081
Sequence 2136, Application US/09617081
GENERAL INFORMATION:
APPLICANT: Gearing, Douglas A.,
APPLICANT: Gearing, Douglas A.,
TITLE OF INVENTION: NUCLEIC ACID MOLECU
TITLE OF INVENTION: HUMAN MAMMARY EPITH
FILE REFERENCE: 1600.1146-001
CURRENT APPLICATION NUMBER: US/09/617,08
CURRENT ETLING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/143,929

MOLECULES DERIVED

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LENGTH: 1991
TYPE: DNA
ORGANISM: HOMO Sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 221818.6
US-60-278-258-16055
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US-60-278-258-16055
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GENERAL INFORMATION:

APPLICANT: Moris, MacDonald

APPLICANT: Lal, Preeti

APPLICANT: Lal, Preeti

APPLICANT: Lal, Preeti

APPLICANT: Lal, Preeti

APPLICANT: Diep, Dinh

TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Us

TITLE OF INVENTION: Polymorphisms Identified Thereby

TITLE OF INVENTION: Polymorphisms Identified Thereby

FILE REFERENCE: GX-0010-1 p

CURRENT FILTING, DATE: 2001-03-23

NUMBER OF SEO ID NOS: 17730

SEO ID NO 16055

LENGTH: 1991

TYPEF. NA.
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Best Local Similarity 99.9%;
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               AGCTTCCTTGAACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAA 539
                                                                                             GGAGACCGCCATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGC 479
                                                                                                                                                                     CATGTCTGGAGACGGGCTGATGCACGAGGTGGTGAACGGGCCTCATGGAGCGGCCTGACTG
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AGCTTCCTTGAACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAA
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                                                                                                            TTTGTTCTGAGACCCCCACCCCACGAACCAAATCCAAATAAAGTGACATTCCCAGCCTGA 1559
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APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
TITLE OF INVENTION: HUMAN PROSTATE AND BREAST LIBRARIES
FILE REFERENCE: 1600.1088-001
CURRENT APPLICATION NUMBER: US/09/526,996
CURRENT FILING DATE: 2000-03-15
EARLIER APPLICATION NUMBER: 60/125,469
EARLIER FILING DATE: 1999-03-22
EARLIER FILING DATE: 1999-03-22
EARLIER FILING DATE: 1999-03-22
VIMBER OF SEQ ID NOS: 1296
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1216
SEQ ID NO 1216
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2494)
OTHER INFORMATION: n = A,T,C of G
US-09-526-996-1216
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         AGGACCCTTCCTCCTAGGGCTGCAGGGCCTGTCCACAGCTCCTGTGGGGGGTGGAG
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                                                                                   AGGACCCTTCCTTCCCTAGGGCTGCAGGGCCTGTCCACAGCTCCTGTGGGGGTGGAG
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APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: New, Henry
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
APPLICANT: Raimzai, Yalda
FILE REFERENCE: PF-0683 P
CURRENT APPLICATION UNMBER: US/50/125,593
CURRENT FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 12
LENGTH: 1573
TYPE: DAN
ORGANISM: Homo sapiens
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US-60-125-593-12
                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 1573; DB 55; Length 1573; Best Local Similarity 100.0%; Pred. No. 4.1e-3303; Matches 1573; Conservative 0; Mismatches 0; Indels 0;
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-60-125-593-12
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1261 CCACCGCCAGAAGAGCCCTTATGACCCCTGGGCCGCGTTGTGCCTTATGTGTTTTTGCA 1320
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                GTGCAGCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGG
                                                 GTGCAGCCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGG
                                                                                                                          CTGGTGCTGCAACCCGCGCGGCGCGAAGGCCAAGGCCTTGCAGCTCTTCCGGAGTCAC
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                                 CTTGTGCCACTGGAGGAGCCACTGCCCTCTCACTGGACAGTGGTGCCCGACGACGACGTTT
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AGACTCCTCTGGAGAAGGGTGAGAAGGTGGAGGCTATGCTTTGGGGGGGACAGGCCAGAAT 1440
                                                                                                        CCACCGCCAGAAGAGCCCTTATGACCCCTGGGCCGCGCTGTGCCTTAGTGTCTACTTTCCA 1320
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Sequence 19, Application US/09937060A

GENERAL INFORMATION:
APPLICANT: INCYTE PHARMACEUTICALS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: TANG, Y. Tom
APPLICANT: TANG, Y. Tom
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: LU, Dyung Aina M.
APPLICANT: LU, Dyung Aina M.
APPLICANT: LU, Dyung Aina M.
APPLICANT: LU, DYUNG, Janice
TITLE OF INVENTION: REGULATORS OF INTRACELLULAR PHOSPHORYLATION
FILE REFERENCE: PF-0683 PCT
CURRENT APPLICATION NUMBER: US/09/937,060A
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 60/125,593; 60/135,049; 60/143,188
PRIOR APPLICATION NUMBER: 60/125,593; 60/135,049; 60/143,188
PRIOR APPLICATION NUMBER: 00/125,593; 60/135,049; 60/143,188
PRIOR FILING DATE: 1999-03-18; 1999-07-09

NUMBER OF SEO ID NOS: 28
SOFTWARE: PERL Program
SEQ ID NO 19
LENGTH: 1573
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US-09-937-060A-19
Sequence 19, Appl;
GENERAL INFORMATI
APPLICANT: INCYI
                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte II
IS-09-937-060A-19
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Local Similarity 100.0%;
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| US-09-813-206-806
| US-09-784-810A-1
| PCT-USO1-05614-90
| PCT-USO1-05614-90
| US-09-205-258-90
| US-09-205-258-90
| US-09-933-767-90
| US-10-004-860-90
| US-10-023-282-90
| US-10-023-282-90
| PCT-USO1-16450-1180
| PCT-USO1-16450A-1180
| PCT-USO1-16450A-129
| PCT-USO1-16450A-129
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| PCT-USO2-28623-2
| US-09-481-275-5302
                                                                                                                                              NO:
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Pred. No. 4.1
0; Mismatches
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No. 4.1e-303;
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Sequence 1, Appli
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Sequence 118, Appli
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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*CG92_6/ptodata//pna/US08_COMB.seq:*
*CG92_6/ptodata//pna/US08_COMB.seq:*
*CG92_6/ptodata//pna/US08_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US07_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	В	ID	Description
1	1573	100.0	1573	35	US-09-937-060A-19	.Sequence 19, Appl
2	1573	100.0	1573	56	us-60-125-593-12	Sequence 12, Appl
ω	1557.2	99.0	2494	19	US-09-526-996-1216	Sequence 1216, Ap
4	1557	99.0	1991	71	US-60-278-258-16055	Sequence 16055, A
u	1550.8	98.6	1783	ר	PCT-US02-24623-1	Sequence 1, Appli
6	1548:8	98.5	2494	23	US-09-617-081-2136	Sequence 2136, Ap
7	1548.8	98.5	2494	24	us-09-637-886-9797	Sequence 9797, Ap
8	1548.8	98.5	2494	25	US-09-649-163-9696	Sequence 9696, Ap
9	1548.8	98.5	2494	25	US-09-652-126-10026	Sequence 10026, A
10	1548.8	98.5	2494	25	us-09-652-913-10528	Sequence 10528, A
11	1548.8	98.5	2494	25	US-09-652-918-8605	
12	1548.8	98.5	2494	26	US-09-663-784-702	Sequence 702, App
13	1548.8	98.5	2494	27	US-09-699-998-8671	Sequence 8671, Ap
14	1548.8	98.5	2494	28	US-09-710-286-2850	Sequence 2850, Ap
15	1548.8	98.5	2494	28	US-09-716-953-1866	Sequence 1866, Ap
16	1548.8	98.5	2494	29	US-09-726-171-2576	Sequence 25/6, Ap
17	1548.8	98.5	2494	29	US-09-726-787-2250	Sequence 2250, Ap
18	1548.8	98.5	2494	29	US-09-726-791-1318	Sequence 1318, Ap
19	1547	98.3	1821	24	US-09-629-469A-13996	· Sequence 13996, A
20	1546.8	98.3	1856	61	US-60-172-373-13168	æ
21	1545	98.2	2440	18	US-09-432-241A-5041	Sequence 5041, Ap
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	14PGREP 618	Db 614
	74 PQQMPPPEEP 383	Оу 374
		Db 559
	14 YECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSWK 373	Оу 314
	99 EGDEVLMLAISPSHLGADLVAAPHAREDDGLVHLCWVRSGISRAALLRLELAMERGSHFS 558	Db 499
		Оу 254
	O GSPKAALHSPVSEGAPVIPPSSGLPLPTPDARVGASTCGPPDHLLPPLGTPLPPDW-VTL 498	Db 440
	25SPVVVQQ	Фу 225
	30 LHRSVSDLPLPLPQPALASPGSPEPLPILSLNGGGPELAGDWGGAGDAPLSPDPLLSSPP 439	Db 380
	25 224	Оу 225
	20 ARFTLGTVLGLATLHTYRGRLSYLPATVEPASPTPAHSLPRAKSELTLTPDPAPPMAHSP 379	Db 320
		Оу 190
	0 LGLDLLLNCSLLLCRGGGHPLDLLSVTLASGSRCFSFLSVAWGFVSDVDIQSERFRALGS 319	Db 260
		Qy 130
	0 SEWDGIVTVSGDGLLHEVLNGLLDRPDWEEAVKMPVGILPCGSGNALAGAVNQHGGFEPA 259	Db 200
	70 GRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQV 129	Oy 7
	O LLPRPPRLLLLVNPFGGRGLAWQWCKNHVLPMISEAGLSENLIQTERQNHARELVQGLSL 199	Db 140
	10 VLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEEL 69	Оу 1
6;	s 195; Conservative 61; Mismatches 107; Indels 127; Gaps	Matches

Search completed: May 9, 2003, 16:53:43 Job time : 50 secs

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RESULT 14
US-60-452-680-12560
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TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-358-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR APPLICATION NUMBER: US 60/382,995
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/385,023
PRIOR APPLICATION NUMBER: US 60/385,023
PRIOR APPLICATION NUMBER: US 60/388,853
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR FILING DATE: 2002-06-17
Sequence 12560, Application US/60452680
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: GRUDE, Andrew
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 78
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Best Local :
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                                                                                                                                                                                                                                                                          614 ----- PGREP 618
                                                                                                                                                                                                                                                                                                                           374 PQQMPPPEEP 383
                                                                                                                                                                                                                                                                                                                                                                                                             314 YECPYLVYVPVVAFRLEPKDCKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSWK 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 DEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHME 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 GSPKAALHSPVSEGAPVIPPSSGLPLPTPDARVGASTCGPPDHLLLPPLGTPLPPDW-VTL 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 LHRSVSDLPLPLPQPALASPGSPEPLPILSLNGGGPELAGDWGGAGDAPLSPDPLLSSPP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 ARFTLGTVLGLATLHTYRGRLSYLPATVEPASPTPAHSLPRAKSELTLTPDPAPPMAHSP 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 LGLDLLLNCSLLLCRGGGHPLDLLSVTLASGSRCFSFLSVAWGFVSDVDIQSERFRALGS 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 THEDLLTHCTLLLCRRLLSPHNILSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGE 189
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hes 195;
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FILING DATE: 2002-04-10
                                                                                                                                                                                                                                                                                                                                                                              LGCPQLGYAAARAFRLEPLTPRGVLTVDGEQVEYGPLQAQMHPGIGTLLTG----PPGC- 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGDFVLMLAISPSHLGADLVAAPHARFDDGLVHLCWVRSGISRAALLRLFLAMERGSHFS 558
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39.8%; Pred. No. 1.6e-74;
ative 61; Mismatches 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 618;
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NESULT 15
US-60-453-135-7839
; Sequence 7839, Application US/60453135
; GENERAL INFORMATION:
                                                                      ; ORGANISM: Homo sapiens US-60-453-135-7839
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US-60-452-680-12560
                                                                                                                       CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7839
LENGTH: 618
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116213
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12560
LENGTH: 618
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                   APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
EILE REFERENCE: CL001456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   614 ----- PGREP 618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380 LHRSVSDLPLPLPQPALASPGSPEPLPILSLNGGGPELAGDWGGAGDAPLSPDPLLSSPP 439
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39.8%;
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Score 886.5; DB 7;
Pred. No. 1.6e-74;
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                      Length 618;
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Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 78
LENGTH: 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1566, 9943,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6188, 21225, 1420, 32236, 2999,
TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 274444, 50566 OR 66428 MOI FORTY
CURRENT APPLICATION: """
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APPLICANT: Millennium Pharmaceuticals, Inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: PCT/US03/02588
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/353,600
PRIOR FILING DATE: 2002-01-31
                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/388,853 PRIOR FILING DATE: 2002-06-14 PRIOR APPLICATION NUMBER: US 60/389,395 PRIOR FILING DATE: 2002-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/371,075
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/371,507
PRIOR FILING DATE: 2002-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/364,517
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                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/374,194 FILING DATE: 2002-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/372,984 FILING DATE: 2002-04-16
                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/385,023 FILING DATE: 2002-05-31
                                                                                                                                                                                                                                                                                                       FILING DATE: 2002-05-24
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/382,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YECPYLYYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSWK 373
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                                                                                                               See
                                                                                                          File Wrapper or PALM
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US-10-354-358-78
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Best Local Similarity
Matches 195; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 78,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                 CURRENT APPLICATION NUMBER: US/10/354,358
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/353,600
PRIOR FILING DATE: 2002-01-31
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                    APPLICANT: Rudolph-Owen, Laura A. TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428, TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428, TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235, TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160, TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469, TITLE OF INVENTION: 8950, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 994, 71TLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099, TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULE FILE REFERENCE: MPIOZ-020PIRROMNIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Millennium Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 DEDFYLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 LHRSVSDLPLPLPQPALASPGSPEPLPILSLNGGGPELAGDWGGAGDAPLSPDPLLSSPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hunter, John Joseph
                                                                                                                                                                                                                                                                                                                                                                                              Williamson, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                              Lesoon, Andrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsai, Fong-Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10354358
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60/371,075
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Pred. No. 1.6e-74;
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US-60-453-135-7837

Sequence 7837, Application US/60453135

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: TAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001456

CURRENT APPLICATION UNMBER: US/60/453,135

CURRENT APPLICATION AND BER: US/60/453,135

CURRENT FILING DATE: 2003-03-10

NUMBER OF SEQ ID NOS: 82762

SOFTWARE: F881SEQ for Windows Version 4.0

SEQ ID NO 7837

LENGTH: 595

TYPE: PRT
                                                                                      ; ORGANISM: Homo sapiens
US-60-453-135-7837
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CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 115213
SOFTMARE: FASTEEQ for Windows Version 4.0
SEQ ID NO 12558
LENGTH: 595
    Overy Match 44.0%; Score 886.5; DB 7; Best Local Similarity 39.8%; Pred. No. 1.5e-74; Matches 195; Conservative 61; Mismatches 107;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 THEDLITHCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFTADVDLESEKYRRLGE 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGCPQLGYAAARAFRLEPLTPRGVLTVDGEQVEYGPLQAQMHPGIGTLLTG----PPGC- 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSPKAALHSPVSEGAPVIPPSSGLPLPTPDARVGASTCGPPDHLLPPLGTPLPPDW-VTL 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.0%; Score 886.5; DB 7; Length 595;
39.8%; Pred. No. 1 5e-74;
1tive 61; Mismatches 107; Indels 127; Gaps
                                         DB 7;
    Indels
                                            Length 595;
  127;
Gaps
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RESULT 11

US-60-453-050-7837

Sequence 7837, Application US/60453050

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele

APPLICANT: CURE, MAY

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES

FILE REPERANCE: CLOO1457

CURRENT APPLICATION NUMBER: US/60/453,050

CURRENT FILING DATE: 2003-03-10

NUMBER OF SEQ ID NOS: 82762

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7837

LENDY: PRT

COUNTY: 595
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Best Local Similarity
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                               130 TNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGE 189
237 LGLDLLLCSLLLCRGGGHPLDLLSVTLASGSRCFSFLSVAWGFVSDVDIQSERFRALGS 296
                                                                                                               177 SEWDGIVTVSGDGLLHEVLNGLLDRPDWEEAVKMPVGILPCGSGNALAGAVNQHGGFEPA 236
                                                                                                                                                                                                                        117 LLPRPPRLLLLVNPFGGRGLAWQWCKNHVLPMISEAGLSFNLIQTERQNHARELVQGLSL 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 LHRSVSDLPLPLPQPALASPGSPEPLPILSLNGGGPELAGDWGGAGDAPLSPDPLLSSPP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297 ARFTLGTVLGLATLHTYRGRLSYLPATVEPASPTPAHSLPRAKSELTLTPDPAPPMAHSP 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 LGLDLLLNCSLLLCRGGGHPLDLLSVTLASGSRCFSFLSVAWGFVSDVDIQSERFRALGS 296
                                                                                                                                                               70 GRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQV 129
                                                                                                                                                                                                                                                                        10 VLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQQMPPPEEP 383
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                                                                                                                                                                                                                                                                                                                                     195; Conservative
                                                                                                                                                                                                                                                                                                                           44.0%; Score 886.5; DB 7; Length 595;
39.8%; Pred. No. 1.5e-74;
htive 61; Mismatches 107; Indels 127; Gaps
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CURRENT APPLICATION NUMBER: US/60/453,135;
CURRENT FILING DATE: 2003-03-10;
NUMBER OF SEQ ID NOS: 82762;
SOFTWARE: FASTSEQ for Windows Version 4.0;
SEQ ID NO 13597;
LENGTH: 307;
TYPE: PRT;
ORGANISM: Homo sapiens
US-60-453-135-13597
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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9811
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US-60-453-135-13597
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Best Local Similarity
Matches 312; Conserv
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                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CARGILL, Michele APPLICANT: IAKOUBOVA, Olga TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001456
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
      198
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Local Similarity 100.0%;
LRLAALRTYRGRLAYLPYGRYGSKTPASPYYYQQGPYDAHLYPLEEPYPSHWTYYPDEDF
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                               EYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSW 372
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nilarity 100.0%;
Conservative (
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; Pred. No. 4.4e-146;
0; Mismatches 0;
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                                                                                                                                                                       Score 1620; DB 7; Pred. No. 5e-144;
                                                                                                                                                         Mismatches
                                                                                                                                                                                      DB 7;
                                                                                                                                                                                      Length 307;
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; Sequence 12558, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARCILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION.
; FILE REFERENCE: CL001450
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 13597
LENGTH: 307
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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AND USES

THEREOF

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Sequence 21, Application US/10348052

Sequence 21, Application US/10348052

GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
APPLICANT: Fyrst, Henrik
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION
TITLE OF INVENTION: OF SPHINGOLIPID METABOLISM AND/OR SIGNALING
FILE REFERENCE: 200116.405
CURRENT APPLICATION NUMBER: US/10/348,052
CURRENT FILING DATE: 2003-01-17
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
SEQ ID NO 21
LENGTH: 368
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-348-052-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 368;
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                              FVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHMEYEC 316
                                                                          FLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDED 240
                                                                                                 FLRLAALRTYRGRLAYLFVGRYGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDED 256
                                                                                                                                                               VMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLT 136
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          MVSGCVEPPPSWKPQQMPPPEEPL 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.4%; Score 1923; DB 6; Length 368; 100.0%; Pred. No. 2e-172;
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RESULT 6
US-09-949-016-9811
Sequence 9811, Application US/09949016
Sequence 9811, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REBERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR REPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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NUMBER OF SEO ID NOS: 2876
SOFTWARE: Patentin Ver. 3.1
SEO ID NO 2585
LENGTH: 333
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Best Local (
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APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PAI31P1

CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR EILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: US/60/205,515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                       172 GFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQ 231
                                                                                                                                                                                                                                                                                                                                                                                                              241 AGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQ
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Conservative 0; Mismatches 0; Indels
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US-10-354-358-26
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                                                                               PRIOR APPLICATION NUMBER: US 60/353,600
PRIOR FILLING DATE: 2002-01-31
PRIOR PFLICATION NUMBER: US 60/364,517
PRIOR FILLING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/371,075
PRIOR APPLICATION NUMBER: US 60/371,507
PRIOR APPLICATION NUMBER: US 60/371,507
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR FILLING DATE: 2002-04-16
PRIOR FILLING DATE: 2002-04-16
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Best Local Similarity
Matches 384; Conserv
                                                                                                                                                                                                                                                                                                APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
TITLE OF INVENTION: 8990, 2100, 9288, 64598, 10480, 20893, 32320, 1586, 9943,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
FILE REFERENCE: MPDIO-2020PIRNOMBIM
CURRENT APPLICATION NUMBER: US/10/354,358
CURRENT FILING DATE: 2003-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Millennium Pharmaceuticals, APPLICANT: Hunter, John Joseph APPLICANT: MacBeth, Kyle J.
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APPLICATION NUMBER: FILING DATE: 2002-0
                                                             APPLICATION NUMBER: US 60/374,194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsai, Fong-Ying
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; ORGANISM: Human US-09-949-016-7026
                                                                                                                                                                                                                                                                                                                                                                                US-09-949-016-7026
                                                                                                                                                                                                                                                                                                                                           Sequence 7026, Application US/09949016 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 26
LENGTH: 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                     SOFTWARE: FastSEQ
SEQ ID NO 7026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 384;
                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/388,853 PRIOR FILING DATE: 2002-06-14 PRIOR APPLICATION NUMBER: US 60/389,395 PRIOR FILING DATE: 2002-06-17
                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed • NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                       PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/385,023 PRIOR FILING DATE: 2002-05-31
                                   LENGTH: 38
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Listing first 45 summaries
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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

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Sequence 26, Appl
Sequence 27, Appl
Sequence 21, Appl
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Sequence 7837, Appl
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Sequence 7839, Appl
Sequence 7839, Appl
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Sequence 7836, Ap
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GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals,
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1 PCT - USO 2 - 31373 - 40 10 US-10-111-896-3 6 US-10-111-896-3 6 US-10-118-140-4 6 US-10-118-140-4 6 US-10-118-140-4 10 US-10-128-1122A-51800 6 US-10-156-761-9811 5 US-09-134-000C-5366 6 US-10-147-884-6786 6 US-10-282-122A-61429 6 US-10-282-122A-61429 6 US-10-282-122A-6143 5 US-09-134-000C-3813 5 US-09-134-000C-3813 6 US-09-134-000C-3813 6 US-09-134-000C-3813 6 US-09-134-000C-3813 6 US-09-134-000C-3813 6 US-09-134-000C-3813 6 US-09-134-000C-3813 7 US-09-134-000C-3813 8 US-09-134-000C-3813
PCT-US02-31373-40 US-10-111-896-5 US-10-111-896-7 US-10-111-996-7 US-10-111-996-7 US-10-282-1120-53800 US-10-156-761-9811 US-09-134-000C-5366 US-10-282-1220-74466 US-10-282-1220-74466 US-10-282-1220-74466 US-10-282-1220-74466 US-09-134-000C-3813 US-09-134-000C-3813 US-09-134-000C-3616 US-09-134-000C-3616 US-09-134-000C-3616 US-09-134-000C-3616 US-09-134-000C-3616 US-09-134-000C-3616 US-09-134-000C-3616 US-09-134-000C-3616

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APPLICANT: HILLENTHUM PHARMACOULICALS, INC.
APPLICANT: HALLENTHUM JOSEPH
APPLICANT: HALLENTHUM JOSEPH
APPLICANT: HALLENTHUM JOSEPH
APPLICANT: LESCON, ANDERS
APPLICANT: LESCON, ANDERS
APPLICANT: MAILLAMSON, MELK
APPLICANTON THE TOWN
TITTLE OF INVENTION: 3703, 1477, 10059, 1660, 1450, 18894, 2088, 3247, 2150,
TITTLE OF INVENTION: 3703, 1477, 10059, 1660, 1450, 18894, 2088, 3247, 2150,
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TITTLE OF INVENTION: 3703, 1477, 10059, 1660, 2089, 3320, 1566, 9943,
TITTLE OF INVENTION: 2150, 26583, 2784, 85285, 10097, 1384, 9925, 14124, 4465,
TITTLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULE
CURRENT FILING DATE: 2000-01-30
PRIOR FILING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: US 60/355,600
PRIOR APPLICATION NUMBER: US 60/371,075
PRIOR APPLICATION NUMBER: US 60/371,075
PRIOR APPLICATION NUMBER: US 60/371,507
PRIOR APPLICATION NUMBER: US 60/372,984
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Sequence 2585, Application PC/TUS0116450

SEQUENCE 2585, Application PC/TUS0116450

SEQUENCE 2585, Application: Inc.

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA131PCT

CURENT APPLICATION NUMBER: PCT/US01/16450

CURENT FILING DATE: 2001-06-01

PRICE APPLICATION NUMBER: 607/205,515

PRICE FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2820

SOFTWARE: PATECHTION VET. 2.0

SEC ID NO 2585

LENGTH: 333

TYPE: PRT

CRCANISM: Homo sapiens
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100.0%; Pred. No. 8.7e-176;
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Sequence 2585, Application PC/TUS0116450A
SEQUENCE INFORMATION:
CEMBERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA131PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens PCT-US01-16450A-2585
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CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2820
SOFTWARE: PATENTLY Ver. 2.0
SEQ ID NO 2555
LENGTH: 333
TYPE: PRT
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301 GQVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL 333
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Sequence 2, Application US/09784810A
GENERAL INFORMATION:
APPLICANT: RASTELLI, LUCA
TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES .
TITLE OF INVENTION: SAME
FILE REFERENCE: 10716-08
CURRENT APPLICATION NUMBER: US/09/784,810A
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,360
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Best Local Similarity 99.2
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SOFTWARE: PatentIn version
SEQ ID NO 3
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DATABASE ACCESSION NUMBER: AFF73423
DATABASE ENTRY DATE: 2000-06-01
RELEYANT RESIDUES: (1)..(384)
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PAGES: 81-84
DATE: 2000
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AUTHORS: Nava et al.
TITLE: Functional characterization of human
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LOCATION: (1)..(384)
OTHER INFORMATION: DEAD ID NO 3 is the peptide sequence of hSPHK1 in Fig. 3, cor OTHER INFORMATION: nding to amino acid residue 1 to 384 of Homo sapiens SPHK-1 OTHER INFORMATION: DBank sequence Accession Number AAF73423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATABASE ACCESSION NUMBER: AAF73423
DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1)..(384)
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VOLUME: 473
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LENGTH: 384
TYPE: PRT
                                                                                                                                                                                             TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
TITLE OF INVENTION: POLYNUCLECTIDES AND MODULATING AGENTS AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 200116.402c2
CURRENT APPLICATION NUMBER: US/10/053,510
CURRENT FILING DATE: 2002-01-17
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 368
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Best Local Similarity 97.7%;
Matches 375; Conservation
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                                                                                                      Query Match
Best Local s
                                                                                          Matches
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PRIOR APPLICATION NUMBER: 60/191,261
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                  LENGTH: 36
TYPE: PRT
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100.0%; Pred. No. 8e-194;
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Pred. No. 6.3e-198;
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                                                                                          Mismatches
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PRIOR APPLICATION NUMBER: US/09/552,317
PRIOR PELICATION NUMBER: US09/552,317
PRIOR PILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR PPLICATION NUMBER: US09/620,312
PRIOR PPLICATION NUMBER: US09/63,450
PRIOR FILING DATE: 2000-08-31
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR PRIOR DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US09/63,036
PRIOR PRIOR DATE: 2000-10-19
PRIOR PPLICATION NUMBER: US09/727,344
PRIOR FILING DATE: 2000-11-29
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SOFTWARE: Pt_Ft_genes_b Versions 1.0
SEQ ID NO 3325
LENGTH: 384
TYPE: PRT
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APPLICANT: Hyseq Inc
TITLE OF INVENTION: NOVEL Nucleic Acid
FILE REFERENCE: 784FLPCT
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     LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300
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US-09-796-487-3
VS-09ence 3, Application US/09796487
GENERAL INFORMATION:
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PCT-US02-24623-10
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PCT-US02-24623-10
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PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/357,501
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 384
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Best Local:
APPLICANT: Spiegel, Sarah
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
FILE REFERENCE: 07320001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,532
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-05-05
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CURRENT FILING DATE: 2002-08-02
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TITLE OF INVENTION: SPHKS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EXOS-104
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APPLICANT: PITSON, S
APPLICANT: Brian, W
APPLICANT: Pu, XIA
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                                                       SOFTWARE: PatentIn version 3.1 SEQ ID NO 2
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Best Local Similarity
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LENGTH: 384
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                                                                                     PRIOR APPLICATION NUMBER: PCT/AU00/00457
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: AU PO 0339
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: AU PO 1504
PRIOR APPLICATION NUMBER: AU PO 1504
PRIOR APPLICATION DATE: 1999-07-08
RIGHER OF SED ID NOS: 56
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/959,897
CURRENT FILING DATE: 2001-11-13
                                                                                                                                                                                                                                                         APPLICANT: Jennifer, BAMBLE R
APPLICANT: Mathew, VADAS A
TITLE OF. INVENTION: SPHINGOSINE KINASE ENZYME
FILE REFERENCE: PITSON-1
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CURRENT FILLING DATE: 1999-03-18
NUMBER OF SEO ID NOS: 14
SOFTWARE: PERL Program
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ORGANISM: Homo sapiens
FEATURE:
TYPE: PRT
ORGANISM: Homo
                                    LENGTH: 384
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Jennifer, BAMBLE R
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GENERAL INFORMATION:
APPLICANT: Tsai, Fong-Ying
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CANCER USING 49863
FILE REFERENCE: METO2-032P1(M)
CURRENT APPLICATION NUMBER: US/60/364,517
CURRENT FLING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 2
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SEQ ID NO 2
LENGTH: 384
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                                                            NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
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Pred. No. 2.5e-203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09970516
GENERAL INFORMATION:
APPLICANT: Novartis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REFERENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                             Matches 384;
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Sequence 3, Application US/10111729
GENERAL INFORMATION:
APPLICANT: Warner-Lambert
TITLE OF INVENTION: Human sphingosine kinase gene
FILE REFERENCE: A000198PCT
FILE REFERENCE: A000198PCT
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US-60-125-593-5
Sequence 5, Application US/60125593; GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 24
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 3
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APPLICANT: Baughn, Mariah R. APPLICANT: Azimzai, Yalda
                                     APPLICANT: Tang, Y. To APPLICANT: Yue, Henry
                                                         APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
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US-09-629-469A-13997
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Best Local Similarity
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APPLICANT: WAKAMATSU, AI
APPLICANT: NAGAI, KEIICHI
APPLICANT: OTSUKI, TETSUJI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING
FILE REFERENCE: 084335/0123
                           PRIOR PRIOR
                                                       PRIOR APPLICATION NUMBER: JP 1999-248036
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 1999-300253
PRIOR FILING DATE: 1999-08-27
                                                                                                                CURRENT APPLICATION NUMBER: US/09/629,469/
CURRENT FILING DATE: 2000-07-28
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NUMBER OF SEQ ID NOS: 19025
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APPLICATION NUMBER: JP 2000-183767 FILING DATE: 2000-05-02
                           APPLICATION NUMBER: JP 2000-118776 FILING DATE: 2000-01-11
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HAYASHI, KOJI
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Pred. No. 1.2e-203;
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                                                               SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 384
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SEQ ID NO 15394
LENGTH: 384
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Best Local Similarity
                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                               CURRENT APPLICATION NUMBER: US/09/937,060A
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 60/125,593; 60/135,049; 60/143,188
PRIOR FILING DATE: 1999-03-18; 1999-05-20; 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/159,590
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 60/183,322
PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                               APPLICANT: AU-YOUNG, Janice
TITLE OF INVENTION: REGULATORS OF
FILE REFERENCE: PF-0683 PCT
                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                 NUMBER OF SEQ ID NOS:
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                                TYPE: PRT ORGANISM: Homo sapiens
NAME/KEY: misc_feature
                  FEATURE:
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BAUCHN, Mariah I
AZIMZAI, Yalda
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TANG, Y. Tom
YUE, Henry
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                  /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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neducary upper	Segmence 5 appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 15394, A	Sequence 13997, A	Description

ALIGNMENTS

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US-09-629-469A-13997

Sequence 13997, Application US/09629469A

GENERAL INFORMATION:
APPLICANT: OTA, TOSHO
APPLICANT: ISGAI, TAKAO
APPLICANT: ISGAI, TAKAO
APPLICANT: ISGAI, TAKAO
APPLICANT: ISATTO, KAORU
APPLICANT: SAITO, KAORU
APPLICANT: SAITO, KAORU
APPLICANT: SAITO, KAORU
APPLICANT: SIGHI, SHIZUKO
APPLICANT: WAKAMATSU, AI
APPLICANT: WAKAMATSU, AI
APPLICANT: NAGAI, KEIICHI
APPLICANT: NOBASS/0123
CURRENT APPLICATION NUMBER: US/09/629,469A
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: JP 1999-248036
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-09
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; ORGANISM: Caenorhabditis elegans
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                                                                                                                                                                               327 FRLEPKDGKGVFAVDGELMVSEAVQ 351
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376 MKLEVISEGSHVVLDGEVVDTKTIE 400
                                                                                                                                                   228 - VVQQGPVDAHLVPLEEPVPSHW------TVVPDEDFVLVLALLHSHL 268
                                                         318 AADGPFAPSAKLEDNRIHLSYILWKDIGTRVNIAKYLLAIEHETHL--DLPFVKHVEVSS 375
                                                                             269 GSEMFAAADMGRCAAGVMHLFYV--RAGVSRAMLLRLFLAMEKGRHMEYECDYLVYVDVVA 326
                                                                                                                     258 KVKTNGSVSDSEEETMETKFQNWTLPDSDETLAVGSSDLEETVVIEDNFVNIYAVTLSHI 317
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Search completed: May 9, 2003, 16:54:15 Job time: 39 secs

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RESULT 14
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Sequence 14, Application US/09817676A
Patent No. US20020042101A1
GENERAL INFORMATION:
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Sequence 4, Application US/09970516
Patent No. US20020099029A1
GENERAL INFORMATION:
APPLICANT: No. US20020099029Alartis AG
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Best Local S
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SEQ ID NO 14
LENGTH: 618
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TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning.
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Spiegel, Sarah
APPLICANT: Kohama, Takafumi
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TYPE: PRT
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Local Similarity 39.8%; Pred. No. 4.3e-78;
nes 195; Conservative 61; Mismatches 107; Indels 127; Gaps
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RESULT 15
US-09-784-810A-15
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; ORGANISM: Homo sapiens
US-09-970-516-4
APPLICANT: RASTELLI, LUCA
TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME:
FILE REFERENCE: 10716-08
CURRENT APPLICATION NUMBER: US/09/784,810A
CURRENT APPLICATION NUMBER: 60/182,360
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION UMBER: 60/182,360
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
PRIOR APPLICATION NUMBER: 60/191,261
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEO ID NOS: 29
SOFTMARE: PATEMENT Ver. 2.1

SEO ID NO 15
LENGTH: 415
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44.0%; Score 886.5; DB 10; Length 618;

Best Local Similarity 39.8%; Pred. No. 4.38-78;

Matches 195; Conservative 61; Mismatches 107; Indels 127; Gaps
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US-09-796-487-9
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Patent No. US20020042358A1
GENERAL INFORMATION:
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                                                                                                                                                                     Matches
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Best Local
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PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: US 09/530,868
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ. ID NOS: 17
                                                                                                                                                                                                                         NAME/KEY: MISC_FEATURE LOCATION: (1)..(204) OTHER INFORMATION: Corr-09-796-487-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and FILE REFERENCE: 0/320001aa (2033957-0001) CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Spiegel, Sarah
                                                                                                                                                                                                                                                                                                                                 LENGTH: 204
TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                             OTHER INFORMATION: Putative kinase sequence obtained by OTHER INFORMATION: everal human ESTs (accession numbers OTHER INFORMATION: 081152 and AA026479).
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                                                               DGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYE-----
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US-09-817-676A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09817676A Patent No. US20020042101A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Mammalian Sphingosine FITTLE OF INVENTION: Expression and Methods FILE REFERENCE: 00170/HG CURRENT APPLICATION NUMBER: US/09/817,676A CURRENT FILING DATE: 2001-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/194,318 PRIOR FILING DATE: 2000-04-03 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Spiegel, APPLICANT: Kohama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                         SEWEGIVTVSGDGLLYEVLNGLLDRPDWEDAVRMPIGVLPCGSGNALAGAVSHHGGFEQV
                                                                                                                                                                                                                                                                                                                                                                                                        NALKTAQLSPIAEGPPEMPASSGFLPPTHSAPEASTWGPVDHLLPPLGSPLPQDWVTIEG
                                                                                                                                                                                            LHRSVSDLPLPLPQPALVSPGSPEPLPDLSLNGGGPELTGDWGGAGDAPLSPDPLLPSSP
                                                                                                                                                                                                                                                          ARFTLGAVLGLASLHTYRGRLSYLPATTEPALPIPGHSLPRAKSELVLAPAPAPAATHSP
                                                                                                                                                                                                                                                                                            MRFTLGTFLRLAALRTYRGRLAYLPV----
                                                                                                                                                                                                                                                                                                                                                       TNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGE 189
GCPHLGYAAARAFRLEPLTPRGLLTVDGELVEYGPIQAQVHPGLATLLTG---
                    ECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSWKP 374
                                                                 E-FYLMLGILTSHLCADLMAAPHARFDDGVVHLCWVRSGISRAALLRIFLAMEHGNHFSL
                                                                                              EDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHMEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.3%;
                                                                                                                                                              -KTPAS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 893; DB 10;
Pred. No. 9.9e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                          PVVVQQGPVDAHLVPLEEPVPSHWTVVPD
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     PAGOKP
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375 Q

Best Local Similarity Matches 307; Conserva

Conservative

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APPLICANT: Spiegel, Sarah
TITLE OF INVENTION: Sphingosin Kinase, Cloning, Ext
FILE REFERENCE: 0732001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,532
PRIOR APPLICATION NUMBER: US 60/186,532
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIA VARSHOLD 3.1
SEQ ID NO 4
LENGTH: 381
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09796487 Patent No. US20020042358A1
                                                                                                                                                                                                                                                                                  NAME/KEY: MISC_FEATURE
LOCATION: (1):.(381)
OTHER INFORMATION: SEO ID NO 4 is the peptide sequence of mSPHKla in Figure 3, corre
OTHER INFORMATION: sponding to amino acid residue 124 to 504 of SPHKla of Genbank sed
OTHER INFORMATION: quence Accession Number AF066748. SEO ID NO 4 is equivalent to SEO
OTHER INFORMATION: O ID NO 1 that is the amino acid sequence of SPHKla in Figure 1.
PUBLICATION INFORMATION:
AUTHORS: Kohama et al.,
TITLE: Molecular cloning and functional characterization of murine sphingosine
TITLE: Kinase
                    DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (124)..(504)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC61697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 DAPSGRDSRRGPPPEEP 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPPPSWKPQQMPPPEEP 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVP 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRR 186
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                                                                                                                                                                                                                                                             Journal of Biological Chemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.48;
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3; Mismatches 36;
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                                                                                                                                   DATABÁSE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
; RELEVANT RESIDUES: (132)..(504)
US-09-796-487-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Spiegel, Sarah

TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use

FILE REFERENCE: 07320001aa (2033957-0001)

CURRENT APPLICATION NUMBER: US/09/796,487

CURRENT FILING DATE: 2001-03-02

PRIOR APPLICATION NUMBER: US 60/186,532

PRIOR FILING DATE: 2000-03-03

PRIOR FILING DATE: 2000-03-03

PRIOR FILING DATE: 2000-05-05

SOFTWARE: Patentin version 3.1

SEO ID NO 5

LENGTH: 373

TYPE: DET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09796487
Patent No. US20020042358A1
GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
                    Query Match 79.8%;
Best Local Similarity 81.3%;
Matches 304; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                       LOCATION: (1)..(373)
OTHER INFORMATION: SEQ ID NO 5 is the peptide sequence of Mouse SPHKla in Fig. 2, OTHER INFORMATION: rresponding to amino acid residue 131 to 504 of SPHKla of GenB OTHER INFORMATION: sequence Accession Number AAC61697.
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 SHWTVVPEQDFLLVLVLLHTHLSSELFAAPMGRCEAGVMHLFYVRAGVSRAALLRLFLAM
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81.4%; Pred. No. 7.4e-151;
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                                               Score 1609.5; DB 10; Pred. No. 4.1e-149;
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RESULT 9 US-09-796-487-4

GENERAL INFORMATION:

ISSUE: 37 PAGES: 23722-23728 DATE: 1998

JOURNAL: JOU VOLUME: 273

ORGANISM: Mus musculus FEATURE:

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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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LOCATION: (1)..(388)
OTHER INFORMATION: SEQ ID NO 2 is the peptide sequence of SPHK1b in Fig. 1, corresponding Information: nding to amino acid residue 1 to 388 of SPHK1b of GenBank sequence OTHER INFORMATION: e Accession Number AAC61698.

PUBLICATION INFORMATION:
AUTHORS: Kohama et al.
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DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (1)...(388)
PUBLICATION INFORMATION:
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DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (1)..(388)
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                                     tch 80.9%; Score 1630.5; DB 10; Length 388; al Similarity 81.7%; Pred. No. 3.9e-151; 308; Conservative 32; Mismatches 36; Indels 1;
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DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (124). (504)
US-09-796-487-1
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US-09-796-487-1
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TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods of Use
FILE REFERENCE: 07320001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT FILING DATE: 2001-03-02
CURRENT FILING DATE: 2001-03-02
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PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: US 09/530,868
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
                                                                                              DATABASE ACCESSION NUMBER: AAC61697
DATABASE ENTRY DATE: 1998-09-26
RELEVANT RESIDUES: (124)..(504)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC61697
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC_FEATURE LOCATION: (1)..(381)
OTHER INFORMATION: SEQ·ID NO 1 is the peptide sequence of SPHKla in Figure 1, cor OTHER INFORMATION: ponding to amino acid residue 124 to 504 of SPHKla of GenBank OTHER INFORMATION: uence Accession Number AAC61697. SEQ ID NO 1 is equivalent to OTHER INFORMATION: ID NO 4 that is the amino acid sequence of mSPHKla in Figure 3
                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 381
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                              ISSUE: 37
PAGES: 23722-23782
DATE: 1998
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                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS: Kohama et al
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80.7%;

Score

1627.5; DB 10;

Length

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; TYPE: PRT
: ORGANISM: Mus musculus
US-09-970-516-6
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US-09-970-516-6
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                                                                                                                                           GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: No. US20020099029Alartis AG

APPLICANT: No. US20020099029Alartis AG

TITLE OF INVENTION: Induction of blood vessel formation through administration of

TITLE OF INVENTION: polynucleotides encoding sphingosine kinases

FILE REFERENCE: 4-31617

CURRENT APPLICATION NUMBER: US/09/970,516

CURRENT APPLICATION NUMBER: 2001-10-04

NUMBER OF SEQ ID NOS: 6

SOFTMARE: PatentIn version 3.1

SEQ ID NO 6

ENCOTH: 382
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Best Local S
Matches 310
Query Match
Best Local Similarity
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CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,360
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/191,261
PRIOR FILING DATE: 2000-03-22
NUMBER FILING DATE: 2000-03-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 29
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80.9%; Pred. No. 5e-152;
ative 33; Mismatches 39; Indels 1;
  81.0%;
80.7%;
  Score 1632.5; DB 10; Length 382; Pred. No. 2.4e-151;
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US-09-817-676A-15
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CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/194,318
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09817676A
Patent No. US20020042101A1
                                                                                                                                                 Matches
                                                                                                                                                                                    Query Match
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PUBLICATION INFORMATION:
TITLE: Molecular cloning and functional characterization
TITLE: murine sphingosine kinase
JOURNAL: J. Biol. Chem.
VOLUME: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Spiegel, Sarah APPLICANT: Kohama, Takafumi TITLE OF INVENTION: Mammalian Sphingosine Kinase Type 2 Isoforms, Cloning, TITLE OF INVENTION: Expression and Methods of Use Thereof FILE REFERENCE: 00170/HG
                                                                                                                                                                                                                                            ISSUE: 37
PAGES: 37722-23728
DATE: 1998-09-11
DATABASE ACCESSION NUMBER: AAC61698
DATABASE ENTRY DATE: 1998-09-26
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                                                            67 EELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGY 126
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                                                                                                                                                 308;
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                                                                                                                                                                 Similarity
                                                                                                                                              Conservative
                                                                                                                                          80.9%; Score 1630.5; DB 10; Lengt 81.7%; Pred. No. 3.9e-151; tive .32; Mismatches 36; Indels
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                                                                                                                                                                                    DB 10; Length 388;
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RESULT 2
US-09-796-487-3
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LENGTH: 384
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TITLE OF INVENTION: Sphingosin Kinase, Cloning, Expression and Methods
FILE REFERENCE: 07320001aa (2033957-0001)
CURRENT APPLICATION NUMBER: US/09/796,487
CURRENT FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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PRIOR EILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: US 09/530,868
PRIOR EILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
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DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1). (384)
PUBLICATION INFORMATION:
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TYPE: PRT
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DATABASE ENTRY DATE: 2000-06-01
RELEVANT RESIDUES: (1)..(384)
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DATE: 2000
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Similarity 99.2%;
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Pred. No. 4.6e-188;
2; Mismatches 1;
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LENGTH: 384
Sequence 4, Application US/09784810A Patent No. US20020082203A1
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CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,360
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 60/191,261
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
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Pred. No. 1.4e-183;
2; Mismatches 7;
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2: //cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: //cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: //cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: //cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
6: //cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
6: //cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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15: //cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
16: //cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                   Length
     BG
US-09-970-516-2
US-09-796-487-3
US-09-784-810A-4
US-09-784-810A-4
US-09-796-487-2
US-09-796-487-1
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Sequence 2, Application US/09970516

Patent No. US2002099029A1

GENERAL INFORMATION:

APPLICANT: No. US2002009029A1artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of the province of US-09-970-516-2 Matches 384; Query Match Best Local Similarity 241 LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300 61 RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETATQKPLCSLDFAGSGNALAASL 120 SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240 LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 100.0%; Score 2016; DB 10; ilarity 100.0%; Pred. No. 7.5e-189; Conservative 0; Mismatches 0; Indels 0; Length 384; 300 0

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 590
TYPE: PRT
ORGANISM: human
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GENERAL INFORMATION:
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APPLICANT: Borges, Luis
TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
TITLE OF INVENTION: Like Receptors (LIR)
FILE REFERENCE: 2624-A
CURRENT APPLICATION NUMBER: US/09/310,463A
CURRENT FILING DATE: 1999-05-12
EARLIER APPLICATION NUMBER: 08/842,248
EARLIER APPLICATION NUMBER: 08/842,248
EARLIER FILING DATE: 1997-04-24
NUMBER OF SED ID NOS: 39
APPLICATION NUMBER: US/08/842,248A FILING DATE: April 24, 1997 CLASSIEICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: Henry, Janls C. REGISTRATION NUMBER: 34,347 REFERENCE/DOCKET NUMBER: 2624 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cosman, David J.
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM/COMPATIBLE
COMPATING SYSTEM: Microsoft Word 7.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry, In
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cosman, David J.

TITLE OF INVENTION: Family of Immunoregulators Designated
TITLE OF INVENTION: Leukocyte Immunoglobulin-Like Receptors (LIR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422
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                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 -DAHLVPL-EEPVPSHWTVVPDEDFVLVLAL----LHSHLGSEMFAAPMGRCAAGVMHL 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --VVTGVSVAFVLLLFLLLFLLLRHRHQSKHRTSAHFYRPAGAAGPEPKDQGLQKRASPV 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDPSLSPTGSTPTPG-----PEDQPLTPTGLDPQSGLGRHLG------ 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Henry, Immunex Corporation
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TELEPHONE: (200) 38'-043' INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: SEQUENCE CHA																	
Indels 88; G KTPASP-VVVOGGPV	1427 LDPAGTVLVTGGTGELGÓAIAAHLVRAHGVRHL 59HARELVRS-EELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIOKPLC	1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPL	4.3%; Score 86; DB 4; Length 6095; cal Similarity 23.4%; Pred. No. 33; 64; Conservative 29; Mismatches 82; Indels	SEQ ID NO 2 LENGTH: 6095 TYPE: PRT ORGANISM: Sorangium S-09-144-085-2	FILING DATE: 1998-08-3 APPLICATION NUMBER: 09, FILING DATE: 1998-01-2: F SEQ ID NOS: 8 F Patentin Ver. 2.0	Ziermann, Rainer vrention: Sorangium PolyKetiDe SYNTHASES AND vvention: Therefor suce: 30062-20020.20 plication NUMBER: US/09/144,085	APPLICANT: GUSTAfsson, Claes APPLICANT: GUSTAfsson, Claes APPLICANT: Betlach, Mary C. APPLICANT: Ashley, Gary APPLICANT: Julien, Bryan	S-09-144-085-2 S-09-144-085-2 Sequence 2, Application US/0914408 Patent No. 6280999	2111.41	374 PQQMPPPEEP : 573 -OEREPPAEP	517 ADIQEEILNAAVKDTQPKDGVEMDARAAASEAPQDVTY	334	288 FYVRAGVSRAMLLRLEL- : 459VVTGVSVAFVLLLELL	. 235 -DAHLVPL-EEDVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMG	182 EKYKRIJSEMKETUGTELKLAALKTYKGKLAYLPYGKYGSNTPASP-Y :	Query Match Best Local Similarity 24 Matches 62; Conservativ	TELEPHONE: (200) 303-0644 TELEPA: (206) 233-0644 TELEPA: 756822 INFORMATION FOR SEQ ID NO: 22 SEQUENCE CHARACTERISTICS: LENGTH: 590 amino acids TYPE: amino acids TYPE: amino acids TYPE: protein MOLECULE TYPE: protein 08-842-248A-22
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CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 18
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Best Local :
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APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: McDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
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309 IPAGDTVLVV-LADAHRTPEREPDP------HRFDIRRDTAG------HLAFGHGIH 352
                                                                                                                                                                                                                                                                                                                                                                                                                                    119 LRPRVQEIVDGLVDAMLAAPDGRADLMESLAWPLPITVISELLGVPEPDRAAFRVWTDAF 178
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                                                  252 VPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRH 311
                                                                                                                                                            194 LGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDA--HLVPLEEPVPSHWTV 251
                                                                                                                                                                                                                                                                    134 LUTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEMRFT 193
                                                                                                                                                                                                                                                                                                                             179 VFP--DDPAQAQTAMA----EMSGYLSRLIDSKRGQDGEDLLSALVRTSDEDGSRLTSEE 232
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                                                                                                          ----QLAALRADMTLLD----GAV-----EEMLRYEGPVESATYRFPV-EPVDLDGTV 308
                                                                                                                                                                                                                     LLGMAHILLVAGHETTVNLI----ANGM-----YALLSHPD------ 264
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Sequence 39, Application US/09105537A

Patent No. 6265202

GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Nao, L.
APPLICANT: Nao, L.
APPLICANT: Nao, L.
APPLICANT: Nao, L.
CUREENT ENCE: 600.438US1

CURRENT APPLICATION NUMBER: US/09/105,537A

CURRENT FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FASTSEQ for Windows Version 3.0

1 ENCRUM: A16

SEQ ID NO 39

SEQ ID NO 316
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: TYPE: PRT
: ORGANISM: Streptomyces venezuelae
US-09-105-537-39
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Best Local (
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403 IRWR 406
                                                   370 PSWK 373
                                                                                                   353 FCIGAPLARLEARIAVRALLERCPDLALDVSPGELV-----WYPNP--MIRGLKALP 402
                                                                                                                                                      312 MEYECPYLVYVPVVAFR--LEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCVEPP 369
                                                                                                                                                                                                      309 IPAGDTVLVV-LADAHRTPERFPDP------HRFDIRRDTAG------HLAFGHGIH 352
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                                                                                                                                                                                                                                                                                                             265 -----QLAALRADMTLLD-----GAV------EEMLRYEGPVESATYRFPV-EPVDLDGTV 308
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US-09-310-463-22 (S-09-310-463-22 ; Sequence 22, Application US/09310463A ; Patent No. 6384203 ; GENERAL INFORMATION:

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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and
FILE REFERENCE: 600. 438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ.ID.NO.37
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APPLICANT: MOCTE, K.

APPLICANT: MAG16, D.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FO

TITLE OF INVENTION: OF BODY WEIGHT DISORDERS IN

FILE REFERENCE: 7853-136

CURRENT APPLICATION NUMBER: US/09/245,041

CURRENT FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: 60/093,630

EARLIER FILING DATE: 1998-07-21
                                                                                                                                                                                                                              US-09-245-041-15
                                                                                                                                                                                                                                                 RESULT 9
                                                                                                                                                                     Sequence 15, Application US/09245041 Patent No. 6274339 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                           266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 DGLMHEVVNGLMERPDWETAIQKPLCSL ------
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Local Similarity 22.1%;
nes 65; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                 GRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP--LEEPVPSHWTVVPDEDFVLVLALLH 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IADVDLESEKYRRLGEMRFTLGTFLRLAA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   %; Score 86.5; D
%; Pred. No. 2.7;
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----HTASGREAVAETGLAWGP 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
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                                                                                               FOR THE DIAGNOSIS AND TREATMENT INCLUDING OBESITY
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                                                                                                                     Вb
                                                                                                                                                                                                                                                                           ; ORGANISM: Streptomyces venezuelae US-09-105-537-6
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EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 131
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                               Query Match 4.3%;
Best Local Similarity 22.1%;
Matches 65; Conservative 1
                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09105537A Patent No. 6265202
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Matches 68; Conserv
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                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin
FILE REFERENCE: 600.438US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 27
TYPE: PRT
                                                                                                                     11104 DGGQHRLTTSLAEA--WANGLALDWASLLPATGALSPAVPDLPTYAFQHRSYWISPAGPG 11161
                                                                                                                                                                                                                                                                                                              LENGTH: 11877
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2746 GRSV 2749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2686 SFVWIQAFVNMYNLASITLMIWSKYCKLFHCGDCGCYTYIDCNFLVFFVLNNSFKQEQEN 2745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2573 FLELAILRTQPGRQRPPGLRACPAYLLKCLPHPNL---APAIAVVSRPGP-PRDIAPESN 2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2541 NARVVTEMKILELKQNPSPHTPV---IPGDLSLWW-----
                                                                              114
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                                                                                                                                                          81 DGLMHEYVNGLMERPDWETAIQKPLCSL--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 WETAIQKPLCSLPAGSGNALAASLNHYAG-----YEQVTNEDLLTNCTLLL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLPTRRCFEMERKIGTSSFKGSNGIDFQLNLCTKHSK--HSLFRTNSGSGNVFVL-LFTI 2685
                                                                              NALAASLNHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---YVRAGVSRAML--
IADVDLESEKYRRLGEMRFTLGTFLRLAA-
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                                                                                                                                                                                           17; Mismatches
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Pred. No. 8.5;
4; Mismatches 101;
                                                                                                                                                                                                                 Score 86.5;
Pred. No. 82;
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                                                                                                                                                                                                                                    DB 4; Length 11877;
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                                         -HTASGREAVAETGLAWGP 11183
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                                                                                                                                                          ------PAGSG 113
                                                                                                                                                                                                 Indels 131;
                                                                                                                                                                                             Gaps
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564 TTAELLVQRFASIDELAAATIDELAALEGVGPITAESIANWFRVEDNRRLIEELKELGVN 623

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US-08-936-135-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.5%; Score 91; DB 3; Length 2584; Best Local Similarity 22.5%; Pred. No. 2.3; Matches 67; Conservative 44; Mismatches 123; indels 64; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
STRANDEDNESS: s:-
TOPOLOGY: ''
TOPOLOGY: ''
TOPOLOGY: ''
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/936,135
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Semaphorin Receptors NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tessier-Lav
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
2265 LASPCYS-ALALYSPRTHRASPLEASP------LYSLYSASNTHRGLILELYSILE 2313
                                                                                              2205 YLYSGLYASNLEGLYGLYILEALAVALASPASPILESERILEASNASNHISILEPRGLNG 2264
                                                                                                                                                                                             2160 LEHISLYSSERLELYSL-------ETYRGLNVALILEPHEGLGLYGLILEGL 2204
                                                                                                                                                                                                                                                                                        2105 NLEVALTRPMETVA-----LVALGLYHISGLNGLYASPHISTRPLYSGLGLYARGVALLE 2159
                                                                                                                                                                                                                                                                                                                                                                                    2049 LYSERHISVALGLYTHRLEARGVALLYSLEHISTYRGLNLYSPRGLGLTYRASPGL---- 2104
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CITY: HILLSBOROUGH
STATE: CALIFORNY.
                                               250 TVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAME 307
                                                                                                                                                                                                                                            150 MNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLG-----EMRFTLGTF-LRLAAL 203
                                                                                                                                           204 RTYRGRLA-----YLPVGRVGSKTPASPVVVQQGPVDA----HLVPLEEPVPSHW 249
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                                                                                                                                                                                                                                                                                                                                        96 DWETAIQKPLCSLPAGSGNALAASLNHYAGYE-----QVTNEDLLTNCTLLLCRRLLSP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                   41 LLAEAEISFTLMLTERRNHARE --- LVRSEELGRWDALVVMS -- GDGLMHEVVNGLMERP 95
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5. 6054293
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CURRENT APPLICATION NUMBER: US/09/182,024A
CURRENT PILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/063,946
PRIOR FILING DATE: 1998-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR RPLICATION NUMBER: 60/096,420
PRIOR FILING DATE: 1998-08-13
NUMBER: 05 SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 1908-10-21
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                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-182-024A-2
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US-09-182-024A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Connolly, Timothy
APPLICANT: Rejput, Bhanu
TITLE OF INVENTION: Human Slit Polypeptide and Polynucleotides Encoding
TITLE OF INVENTION: Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6380370
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SEQ ID NO 5553
LENGTH: 319
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                                                                                                                                                                                                                                                     Query Match 4.3%; Score 87; DB 4; Length 1523; Best Local Similarity 24.2%; Pred. No. 2.9;
                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
793 YTFSNMSHLSTLILSYNRLRCIPVHAFNGLRSLRVLTLHGNDISSVPEGSFNDLTSLSHL 852
                                                       145 RLLSPMNLLS------LHTASGLRLFSVLSLAWGFIADV-----DLESEKYR 185
                                                                                                               733 ETVVRCSNKGLRALPRGMPKDVTELYLEGNHLTAVPRELSALRHLTLIDLSNNSISMLTN 792
                                                                                                                                                                   98 ETAIQ---KPLCSLPAG-----SGNALAASLNHYAGYEQVTNEDLLTNCTLLLCR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                watch (Match 23.7%; Score 87.5; DB 4; Length 319; Local Similarity 23.7%; Pred. No. 0.22; Length 319; as 28; Conservative 26; Mismatches 47; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 GDGTLNELVNGVM-----QYQLNLPIGVIPGGTFNDFTKTLQLHPNF-KTASEQLLTS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLTN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 NGIGEVAKSLSSMCKHLSLQLSENKGDIIKYCKSIKNENYSSDV------DVLFILG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 NPRGGKGKALQLFRSHVQPLLAE--AEISFTLMLTERRNHARELVRSEELGRWDALVVMS 79
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                           26; Mismatches 101; Indels
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353 QVHPNY 358 :: |: 285 KLPANF 290

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                                                                                           : NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3782
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-105-537-4
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US-09-412-545-2
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US-09-105-537-4
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LENGTH: 1065
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 4.9%; Score 99.5; DB Best Local Similarity 24.6%; Pred. No. 0.064; Matches 55; Conservative 33; Mismatches
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Patent No. 6255095
Query Match 4.9%; Score 99; DB 4; Length 3782; Best Local Similarity 24.1%; Pred. No. 0.53; Matches 103; Conservative 48; Mismatches 189; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09105537A Patent No. 6265202
                                                                                                                                                                                                                                           APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Prescott, Stephen M.
APPLICANT: Ding, Li
APPLICANT: Traer, Elie
TITLE OF INVENTION: HUMAN DIACYLGLYCEROL KINASE IOTA
FILE REFERENCE: 1321.2.25
CURRENT APPLICATION NUMBER: US/09/412,545
CURRENT FILING DATE: 1999-10-05
EARLIER APPLICATION NUMBER: 60/103,079
EARLIER FILING DATE: 1998-10-05
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     513 EELEDGVCKLPLNVFNNVFSL--GFDAHVTLEFHESREANPEKF 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 PLGTGNDLARTINWGGGY---TDEPV----SKILCQVEDGTVVQLDRWNLHVERNPDLPP 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 PAGSGNALAASLNHYAGYEQVTNEDLLTNCTLLLCR---RLLSPMNLLSLHTASG----- 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404 -RQVFDLSQEGPKDALELYRKVPNLRILACGGDGTVGWILSILDE---LQLSPQPPVGVL 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 PISSP---LMKP--LLVFVNPKSGGNQGTKVLQMFMWYLNP---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 ARELYRSEELGRWDAL-------VVMSGDGLMHEVVNGLMERPDWETAIQKPLCSL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 PAGGPRGVLPRPCRVLVLLNPRGGKG----KALQLFRSHVQPLLAEAEISFTLMLTERRNH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------LRLF-SVLSLAWGFIADVDLESEKYRRLGEMRF 192
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	0	240	RLAYLPVGRVGSKTPASPVVVQQ******GPVDAHLVP		209	ν,
	ω	IRHVGK 56		LED	520	Db
	80	LAALRTYRG 208	NLLSLHTASGLRLFSYLSLAWGFIADVDLESEKYRRLGEMRFT1GTFLRLAALRTYRG	:	151	Qy
	9 0	PM 150 : PLSDLYRLK 519	LPAGSGNALAASLNHYAGYEQVTNEDLLTNCTLLLCRR-LLSPM 		108 460	Qy Db
	9 7	PLCS 107 PSCGSQLVR 459	HARELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCS		59 401	Db 09
	11;	2; 80; Gaps	h 4.6%; Score 93; DB 4; Length 712; Similarity 21.8%; Pred. No. 0.19; 63; Conservative 37; Mismatches 109; Indels	atc cal	Query M Best Lo Matches	
			hodothermus max	e : ∃ 7 0	SEQ ID NO 9 LENGTH: 7 TYPE: PRT ORGANISM: -09-708-426	Ω̈
			11-09 R99-49591 10	APPLIAPPLIA	CURRENT FOR APP PRIOR FIL NUMBER OF SOFTWARE:	
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			9 YE-SUN YEON-GY	H H Z Y	Patent No. GENERAL INF APPLICANT: APPLICANT:	
			9 Application US/09708426	9 (2)	RESULT 4 US-09-708-	US;
			: : DFARSWQP 527		520	Дb
			EPPPSWKP 374		. 367	Qy
	. .	TEWMVSGCV 366	RHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCV 		310 475	Db Qy
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	. 1 3		PMNLLSLHTASG : PVQLDARVVRGETELAG	NALA # : NAVL	114 252	рь
	1 3		ELVRSEELGRWDAL-VVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSG 	ELVR- : : DLLER	62 192	Dp QA
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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1 MDPAGGPRGVLPRPCRVLVL......CVEPPPSWKPQQMPPPEEPL 384
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4 US-09-105-537-4
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Sequence 4774, Ap
Sequence 2, Appli
Sequence 4, Appli
Sequence 9, Appli
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Sequence 37, Appli
Sequence 15, Appl
Sequence 18, Appli
Sequence 18, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 21, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 34, Appli
Sequence 31, Appli
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83 4.1 424 4 US-08-760-79/A-3 83 4.1 424 4 US-08-932-929B-3 83 4.1 435 2 US-08-031-538-1 83 4.1 520 5 PCT-US95-04801-5 82.5 4.1 471 4 US-09-225-256-26 82 4.1 840 2 US-08-500-857A-6 80.5 4.0 2867 1 US-08-500-857A-6 80.5 4.0 2867 2 US-08-462-467B-2 80.5 4.0 1447 3 US-08-462-467B-2 80 4.0 1447 3 US-08-56-055-19 80 4.0 1447 4 US-08-954-668-19 80 4.0 1447 4 US-08-918-658-19	45	44	43	42	41	40	39	38	37	36	35	34	ω G	32	31	30	29	0
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4 US-08-932-9598-3 4 US-08-932-9598-3 5 US-08-931-538-11 5 PCT-US95-04801-5 6 US-09-325-256-26 1 US-09-325-256-26 1 US-08-500-6578-2 2 US-08-5462-4678-2 2 US-08-546-468-19 3 US-08-954-668-19 4 US-08-954-668-19 5 US-08-918-658-19 5 US-08-918-658-19 6 US-08-918-658-19 7 US-08-918-658-19 8 US-08-918-658-19 9 US-08-918-658-19	1117	1117	928	928	1447	1447	1447	1447	1447	1447	2887	287	840	471	520	435	424	424
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	US-09-382-911-6	US-08-841-483-6	US-09-382-911-4	US-08-841-483-4	PCT-US95-13233-19	US-08-918-658-19	US-09-268-140-5	US-08-954-668-19	US-08-656-055-19	US-08-540-406-19	US-08-462-467B-2	US-07-952-817-24	US-08-500-857A-6	US-09-325-256-26	PCT-US95-04801-5	US-08-031-538-11	US-08-932-929B-3	US-U8-/6U-/9/A-3
Sequence 3, Sequence 3, Sequence 11 Sequence 26 Sequence 26 Sequence 19 Sequence 6, Sequen	Appli	Appli	Appli	Appli	19, Appl	19, Appl), Appl	19, Appl	19, App1	App1i	: 24, Appl	Appli	26, Appl	Appli			Trddy

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Matc	nes	Matches 307; Conservative 33; Mismatches 36; Indels 1; Gaps 1;
Оy	7	PRGVLPRPCRYLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRS 66
Db	6	PRGLLPRPCRVLVLLNDQGGKGKALQLFQSRVQPFLEEAEITFKLILTERKNHARELVCA 65
Qy	67	EELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGY 126
Db	66	EELGHWDALAVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPGGSGNALAASVNHYAGY 125
Qy	127	EQVINEDLLINCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRR 186
Db	126	EQVTNEDLLINCTLLLCRRRLSPMNLLSLHTASGLRLYSVLSLSWGFVADVDLESEKYRR 185
Qy	187	LGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVP 246
Db	186	IGEIRFTVGTFFRLASLRIYQGQLAYLPVGTVASKRPAS-TLVQKGPVDTHLVPLEEPVP 244
Оу	247	SHWTVVPDEDEVLVLALLHSHLGSEMEAAPMGRCAAGVMHLFYVRAGVSRAMLLRLELAM 306
DЬ	245	SHWTVVPEQDELLVLVLLHTHLSSELFAAPMGRCEAGVMHLFYVRAGVSRAALLRLFLAM 304
Qy	307	EKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCV 366
da	305	QKGKHMELDCPYLVHVPVVAFRLEPRSQRGVFSVDGELMVCEAVQGQVHPNYLWMVCGSR 364
Qy	367	EPPPSWKPQQMPPPEEP 383
рb	365	DAPSGRDSRRGPPPEEP 381
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Best Local
                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                         kinase content of cells, specifically for reducing cell death and/or increasing cell proliferation; and (b) to produce transfected cells that are used to screen for agents that inhibit or promote sphingosine kinase activity. Agents that reduce sphingosine kinase activity or expression are used: (i) to reduce cell proliferation, specifically for treating cancer, and (ii) to treat diseases associated with abnormal cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the mouse sphingosine kinase la. The coding sequence was isolated by searching a dbEST (expressed sequence tag database) using amino acid sequence results from sequenced tryptic digests of the rat sphingosine kinase. Expression of sphingosine kinase in cells results in formation of sphingosine-1-phosphate, a known second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anticancer; antiproliferative; antiatherosclerotic; stroke; restenosis; antineurodegeneration; sphingosine kinase; cell proliferation; apoptosi cancer; diabetic neuropathy; Alzheimer's disease; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                messenger, and confers serum-independent growth; increases proliferation and suppresses serum-deprivation or ceramide-induced apoptosis. The sphingosine kinase nucleic acid is used: (a) to increase sphingosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New sphingosine kinase, used to treat diseases involving abnormal cell proliferation, e.g. cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-1998;
11-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9961581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                            migration or motility, particularly cancer, restenosis or diabetic neuropathy (but also atherosclerosis, stroke and Alzheimer's disease), whereas agents that stimulate sphingosine kinase can be used to treat conditions associated with reduced cell proliferation, e.g. developmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 1; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DEAN-) OFFICE
 66
                                 67
                                                                                                                             Local Similarity 81.4 es 307; Conservative
                                                                σ
                                                            2000-072612/06
EELGHWDALAVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPGGSGNALAASVNHYAGY
             EELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGY 126
                                                                                                                                                                                                  381
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98US-0096049.
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                                                                                                                                              80.7%;
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                                                                                                                             Score 1627.5; DB 21
Pred. No. 1.9e-167;
3; Mismatches 36;
                                                                                                                                                              DB 21;
                                                                                                                               Indels
                                                                                                                                                            Length 381;
                                                                                                                                                                                                                                              e.g. developmental
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RESULT 15
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                               useful for decreasing cell proliferation, e.g. for treating cancer, and for treating diseases associated with abnormal migration and motility of cells, e.g. restenosis or diabetic neuropathy. Agents that increase activity are used to reduce cell death. Antibodies raised against SPHK, and primers or oligonucleotides derived from the DNA are useful for diagnosis. The antibodies are also useful as therapeutic inhibitors. The present sequence represents a murine sphingosine kinase la (mSPHKla) corresponding to residues 124 to 504 of SPHKla in GenBank Accession no. AAC61697.
                                                                                                                                                                                                 The invention relates to an isolated sphingosine kinase (SPHK) DNA (transformed with SPHK DNA are used to screen for agents that reduce, eliminate or promote SPHK activity. Agents that inhibit activity are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB08087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sphingosine kinase; SPHK; SPHKla; cytostatic; vasotropic; antidiabetic; neuroprotective; mouse; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine sphingosine kinase la (mSPHKla) protein sequence
                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 24pp; English.
                                                                                                                                                                                                                                                                                                                     transformed cells
                                                                                                                                                                                                                                                                                                                                    New isolated sphingosine kinase, useful in identifying modulators treating e.g. cancer, also related nucleic acid, vectors and
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-478846/51
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                                                                                                                                                                                                                                                                                                                                  treating e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SPIE/) SPIEGEL S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAPSGRDSRRGPPPEEP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPPPSWKPQQMPPPEEP 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; protein; 381
                                                                                                                                                                                                                       an isolated sphingosine kinase (SPHK) DNA. Cells A are used to screen for agents that reduce,
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Query Match Best Local Similarity

80.7%; 81.4%;

Score 1627.5; DB 23; Pred. No. 1.9e-167;

Length 381;

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the mouse sphingosine kinase la. The coding CC sequence was isolated by searching a dbEST (expressed sequence tag CC database) using amino acid sequence results from sequenced tryptic CC digests of the rat sphingosine kinase. Expression of sphingosine kinase CC in cells results in formation of sphingosine-1-phosphate, a known second CC messenger, and confers serum-independent growth; increases proliferation, CC and suppresses serum-deprivation or ceramide-induced apoptosis. The sphingosine kinase nucleic acid is used: (a) to increase sphingosine kinase content of cells, specifically for reducing cell death and/or increasing cell proliferation; and (b) to produce transfected cells that CC increasing cell proliferation; and (b) to produce transfected cells that CC are used to screen for agents that inhibit or promote sphingosine kinase activity. Agents that reduce sphingosine kinase activity or expression CC are used to it to treat diseases associated with abnormal cell migration or motility, particularly cancer, restenosis or diabetic conditions associated with reduced cell proliferation, e.g. developmental CC retardation.
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10-SEP-2002 (first entry)
                                            ABB08088
                                                                                    ABB08088 standard;
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N-PSDB; AAZ47168.
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hes 308;
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                                                                                                                                                                                                                                                                                                                                                                                        SHWTVVPDEDFYLVLALLHSHLGSEMFAAPMGRCAAGVMHLEYVRAGVSRAMLLRLELAM 306
                                                                                                                                                                                            DAPSGRDSRRGPPPEEP
                                                                                                                                                                                                                                   EPPPSWKPQQMPPPEEP 383
                                                                                                                                                                                                                                                                                                    EKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCV 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGEMRETLGTELRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGY 126
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                                                                                                                                                                                                                                                                              QKGKHMELDCPYLVHVPVVAFRLEPRSQRGVFSVDGELMVCEAVQGQVHPNYLWMVCGSR 371
                                                                                                                                                                                                                                                                                                                                                                  SHWTVVPEQDFVLVLLHTHLSSELFAAPMGRCEAGVMHLFYVRAGVSRAALLRLFLAM 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGEIRFTVGTFFRLASLRIYQGQLAYLPVGTVASKRPAS-TLVQKGPVDTHLVPLEEPVP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQVTNEDLLINCTLLLCRRRLSPMNLLSLHTASGLRLYSVLSLSWGFVADVDLESEKYRR 192
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                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.9%; Score 1630.5; DB 21; Length 388; B1.7%; Pred, No. 9.4e-168; tive 32; Mismatches 36; Indels 1;
                                                                                      388 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 24pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                no. AAC61698.
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  367 EPPPSWKPQQMPPPEEP 383
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                                                                                                                                                                                                                                                                                                                                                                                     13 PRGLLPRPCRVLVLLNPQGGKGKALQLFQSRVQPFLEEAEITFKL1LTERKNHARELVCA 72
                                                                                                                                                                                                                                                                                                                                                                                                                       7 PRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRS 66
                                                                                                                         SHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAM 306
                                                                                                                                                                                             LGEMRFTLGTFLRLAALRTYRGRLAYLPVGKVGSKTPASPVVVQQGPVDAHLVPLEEPVP 246
                                                                                                                                                                                                                                            QKGKHMELDCPYLVHVPVVAFRLEPRSQRGVFSVDGELMVCEAVQGQVHPNYLWMVCGSR
                                                                    EKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCV 366
                                                                                                        SHWTVVPEQDFVLVLVLLHTHLSSELFAAPMGRCEAGVMHLFYVRAGVSRAALLRLFLAM
                                                                                                                                                                           LGEIRFTVGTFFRLASLRIYQGQLAYLPVGTVASKRPAS-TLVQKGPVDTHLVPLEEPVP
                                                                                                                                                                                                                                                                                                                                                     EELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.9%; Score 1630.5; DB 23; Lengt 81.7%; Pred. No. 9.4e-168; tive 32; .Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 23; Length 388;
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372 DAPSGRDSRRGPPPEEP 388

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The and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; sphingosine kinase; SphK; restenosis; ischaemia; gene therapy; antisense therapy; cancer; sphingolipid; signalling molecule; apoptosis; cytostatic; tumour necrosis factor-alpha; TMF; atherosclerosis; lymphoma leukaemia; vasotropic; cell proliferative disorder; vascular disease.
                                                                                                                                                      An isolated Sphingosine kinase polypeptide useful for treating SphK-associated disorder especially cancer, restenosis or ischauman .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2000;
22-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse consensus sphingosine kinase (SphK) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE07883 standard; Protein; 382
                                                                                             Example 1; Page 92-94; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus
           present invention relates to sphingosine kinase nucleic acids encoding them. SphK is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL 384
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DB; AAD14425.
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Similarity 100.0%;
33; Conservative (
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GENENTECH INC.
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2000US-0191261.
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                 (SphK) polypeptides
treating a SphK-
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                            Anticancer; antiproliferative; antiatherosclerotic; stroke; restenosis; antineurodegeneration; sphingosine kinase; cell proliferation; apoptosi cancer; diabetic neuropathy; Alzheimer's disease; atherosclerosis.
                                                                                                                                                                                                                               Mouse sphingosine kinase 1b protein
                                                                                                                                                                                                                                                         28-MAR-2000
                                                                                                                                                                                                                                                                                                            AAY56054 standard;
                                    26-MAY-1998;
11-AUG-1998;
                                                                           25-MAY-1999;
                                                                                                   02-DEC-1999
                                                                                                                           WO9961581-A2
                                                                                                                                                     Mus musculus
          (DEAN-) OFFICE DEAN RES & GRADUATE
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                                                                                                                                                                                                                                                                                                                                                                           MVCGSRDAPSGRDSRRGPPPEEP
                                                                                                                                                                                                                                                                                                                                                                                                                             RLFLAMQKGKHMELDCPYLVHVPVVAFRLEPRSQRGVFSVDGELMVCEAVQGQVHPNYLW
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                                    98US-0086657.
98US-0096049.
                                                                           99WO-US11521
                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                         entry)
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80.9%;
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                                                                                                                                                                                                                                                                                                             388
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Pred. No. 9.7e-169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                         apoptosis;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 90-91; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An isolated Sphingosine kinase polypeptide useful for treating a SphK-associated disorder especially cancer, restenosis or ischemia in
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                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD14424.
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22-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE07882 standard; Protein; 384 AA
                                                                                                                                                                                                                                                                                                                                                        SphK) protein.
                                                                                                                                61
                                                                                                                                                                61
NHYAGYEQVTNEDILTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                                              MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA 60
                                                              NHYAGYEQVTNEDLLTNCTLLLCRPVLSPMNLLSLHTASGLRSFSVLSLAWGFIADVDLE
                                                                                                                               RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
                                                                                                                                               RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120
                                                                                                                                                                                             MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA 60
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                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                          384 AA;
                                                                                                                                                                                                                                                            Conservative
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2000US-0191261
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                                                                                                                                                                                                                                                                       97.3%;
97.7%;
                                                                                                                                                                                                                                                        Score 1962; DB 22;
pred. No. 1.1e-203;
2; Mismatches 7;
                                                                                                                                                                                                                                                        7; Indels
                                                                                                                                                                                                                                                                                       Length 384;
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABL89940-ABL90844) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, altergies, autoimune chaemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's clisease, multiple sclerosis, rheumatoid arthritis and ucerative disease, multiple sclerosis, rheumatoid arthritis and ucerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epileps; and (f) infectious diseases such as viral, bacterial, fungal and parastic infections.

Claim 11; SEQ ID NO 2585; 2081pp + Sequence Listing; English.

disorders

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format direfrom WIPO at ftp.wipo.int/pub/published_pct_sequences.

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                                                                                                                                                                                                                                                                     Novel 1405 isolated polypeptices, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, qastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antialiergic; hepatotropic; antidiabetic; antiinfiammatory; antiucer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                      WPI; 2002-122018/16
N-PSDB; ABL90618.
                                                                                                                                                                                                                                                                                                                                                          Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human polypeptide SEQ ID NO 2585.
                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-2000; 2000US-205515P
                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-2001; 2001WO-US16450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 MVSGCVEPPPSWKPQQMPPPEEPL 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated sphingosine kinase (SPHK) DNA. Cells transformed with SPHK DNA are used to screen for agents that reduce, eliminate or promote SPHK activity. Agents that inhibit activity are useful for decreasing cell proliferation, e.g. for treating cancer, and for treating diseases associated with abnormal migration and motility of cells, e.g. restenosis or diabetic neuropathy. Agents that increase activity are used to reduce cell death. Antibodies raised against SPHK, and primers or oligonucleotides derived from the DNA are useful for diagnosis. The antibodies are also useful as therapeutic inhibitors. The present sequence represents a human sphingosine kinase 1 (hSPHKI).
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                                                                                       antiinflammatory; antialle:
cancer; therapy; diagnosis
                                                                                                                      Sphingosine kinase A; SKA; human;
                                                                                                                                                   Human sphingosine kinase A
                                                                                                                                                                                   05-DEC-2000
                                                                                                                                                                                                                                              AAY96057 standard; Protein;
                               WO200052173-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isolated sphingosine kinase, useful in identifying modulators ating e.g. cancer, also related nucleic acid, vectors and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
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                                                            sapiens
                                                                                                                                                                                                                                                                                                                         MVSGCVEPPPSWKPQQMPPPEEPL 384
                                                                                                                                                                                                                                                                                                                                                       MVSGCVEPPPSWKPQQMPPPEEPL
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                                                                                                                                                                                   (first entry)
                                                                                                    antiallergic; anticancer;
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                                                                                                                                                                                                                                               A
                                                                                                                       drug
                                                                                                                       screening;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKB and SKC. The polypeptides can be obtained using recombinant DNA methods, and host cells containing expression vectors including SK polypucleotides are used in a claimed method of screening for compounds that inhibit or activate human SK activity. Human SK specific antibodies, inhibitors, ligands or their analogues can be used as bioactive agents to treat inflammation or disease including viral, bacterial or fungal infections, allergic responses, mechanical injury associated with trauma, hereditary diseases, lymphoma or carcinoma, and other conditions with activate the genes of kidney, lung, heart, lymphoid or tissues of the nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an enzyme that phosphorylates sphingosine to form sphingosine 1-phosphate. The sequence was deduced from that of a polynucleotide (see AAA50508) isolated from an HeLa cDNA library. The invention provides polynucleotides (see AAA50508-10) and polypeptides (see AAY96057-59) for the human sphingosine kinase (SK) homologues SKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human sphingosine kinase A, B and C polynucleotides and polypeptides useful in e.g. chromosome and gene mapping, and detecting inflammation or disease associated with abnormal levels of sphingosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2000; 2000WO-CA00223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of human sphingosine kinase A (SKA),
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                                                                                                                                                                          MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA
MVSGCVEPPPSWKPQQMPPPEEPL
                                                               RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFW 360
                                                                                                                              LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL
                                                  RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVRRAVQGQVHPNYFW
                                                                                                             LEEPVPSHWTVVPDEDFYLYLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL
                                                                                                                                                                                                                                                                                                           RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCILPAGSGNALAASL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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99.2%;
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Pred. No. 8e-208;
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MVSGCVEPPPSWKPQQMPPPEEPL

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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and
                                                                                                                                                                                                                                                                                                                                                                                                      Tang
Wang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; cNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                            Example
                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-DEC-2000; 2000WO-US34263
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DB: AAI59336.
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                                                                                                                                                                                   5; SEQ ID NO 3325; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      , Liu C,
Wang Z,
Zhou P,
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0652191.
2000US-0693036.
2000US-0727344.
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Wehrman T, X
, Goodrich R,
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, Xu C, Xue AJ,
R, Drmanac RT;
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Zhang J;
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           Spiegel S;
                                                                        02-MAR-2000; 2000US-186352P
                                         (SPIE/) SPIEGEL S.
                                                                                                    02-MAR-2001; 2001US-0796487
                                                                                                                                    11-APR-2002
                                                                                                                                                                  US2002042358-A1
                                                                                                                                                                                                                                                                          Human sphingosine kinase 1 (hSPHK1) protein sequence
                                                                                                                                                                                                                                                                                                                                                                     ABB08089 standard; protein; 384 AA
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Ote: The sequence data for this patent did not form part of the printed
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Pred. No. 5.1e-209;
0; Mismatches 1;
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Matches 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is human sphingosine kinase type 1 (hsk1). The sk1 gene is located on chromosome 17q25.2. The sk1 converts the substrate sphingosine to sphingosine-1-phosphate (SIP). The sk1 gene and encoded polypeptide are applicable in screening drug candidates particularly inhibitors for preventing or treating disorders such as haemostasis, thrombosis, allergic reactions, proliferative diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sclerosis, T helper-1 related diseases, chronic obstructive pulmonary disease, asthma, myocardial infarction, neurodegenerative disorders,
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07-FEB-2000; 2000US-0180525.
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Local Similarity 100.0%;
nes 384; Conservative 0;
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   LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL
                              | LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL
                                                                                                                   SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
                                                                                                                                              SEKYRRLGEMRETLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
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Pred. No. 1.5e-209;
Mismatches 0;
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121 NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFTADVDLE

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RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL

RELYRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL

MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA

MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAE I SFTLMLTERRNHA

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RESULT 5
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Best Local:
  Matches
                                                                                                   This represents a human sphingosine kinase (SK) protein. The human SK protein, encoding nucleic acids and modulators are useful for modulating expression, functional activity or cellular functional activity of sphingosine kinase in a subject and also for treating a mammal by
                                                                                                                                                                                    Novel sphingosine kinase protein and nucleic acid molecules for diagnosis, prophylaxis and treatment of rheumatoid arthritis, as atherosclerosis, inflammation, meningitis, multiple sclerosis as septic shock
                                                                              modulating the activity of SK. Diseases treated by regulating SK cellular activity include rheumatoid arthritis, asthma, atherosclerosis,
                                                                                                                                                                                                                                           N-PSDB; AAC84161.
                                                                                                                                                                                                                                                                                                                       13-MAY-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sphingosine kinase; antiarthritic; antiinflammatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB48007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB48007 standard; Protein; 384
                                              Sequence
                                                                                                                                                           Claim 9; Fig 7a; 100pp; English.
                                                                                                                                                                                                                                                     WPI; 2001-016227/02
                                                                                                                                                                                                                                                                                                                                                        12-MAY-2000; 2000WO-AU00457
                                                                                                                                                                                                                                                                                                                                                                               23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                     W0200070028-A1
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAR-2001
                                                                   inflammation, meningitis,
                                                                                                                                                                                                                                                                                                 (JOHJ ) JOHNSON & JOHNSON RES PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
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           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sphingosine kinase protein sequence
  383;
       Similarity
                                               384 AA
                                                                                                                                                                                                                                                                           Wattenberg
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                       99AU-0000339.
           99.98;
                                                                                                                                                                                                                                                                           BW,
                                                                   multiple sclerosis and
Score 2013; DB 22;
Pred. No. 3.1e-209;
1; Mismatches 0;
                                                                                                                                                                                                                                                                           Xia P,
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antibacterial;
                                                                                                                                                                                                                                                                           D'Andrea
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                                                                   septic
                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarteriosclerotic;
immunosuppressive;
                                                                                                                                                                                                                                                                           Gamble JR,
  Indels
                       Length
  0
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                                                                                                                                                                                                         asthma,
 Gaps
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                                                                                                                               Ota T, I
                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                                                                                                                                                                                                                          29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                     Human; primer;
                                                                                                                                                                                                                                                                                                                                                                          Human protein sequence SEQ ID NO:15394.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAB94589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB94589 standard; Protein; 384 AA
                      Claim 8; SEQ ID 15394; 2537pp + CD ROM; English
                                                                                                                                                                                                   11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                          28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                         EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2001 (first entry)
The present invention describes primer sets for synthesising 5602
                                                                                                        WPI; 2001-318749/34.
                                                                                                                                                                (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                              Isogai T, Nishikawa T, Hayashi K,
, Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                        2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                          99JP-0248036.
99JP-0300253.
                                                                                                                                                                                                                                                                                                                                                      detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Mismatches 0;
                                                                                                                               Saito K,
K, Otsuki
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Best Local Similarity 100 Matches 384; Conservative
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Best Local
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                                                                                                                                                                       04-JUL-2001 (first entry)
                                                                                                                                                                                                                                                  AAE00924 standard; Protein; 384 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                    RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFW 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
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100.0%; Pred. No. 1.5e-209;
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Human; sphingosine kinase type 1; sk1; chromosome 17q25.2; sphingosine-1-phosphate; SIP; drug screening; therapy; haemostasis; thrombosis; allergio reaction; proliferative disease; cancer; haematopoletic disorder; leukaemia; cardiovascular disease; stroke; atherosclerosis; coronary artery disease; dyslipidaemia; diabetes; autoimmune disease; inflammatory disease; multiple sclerosis;

sphingosine kinase type 1 (hsk1).

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MVSEAV

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                                                         TRANSMEM
DOMAIN
DOMAIN
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15-JUN-2002 (Rel. 41, Last annoctation update)
Semaphorin 4B (Semaphorin C) (Sema C) (Fragment).
SEMA4B OR SEMAC OR SEMC.
           DISULFID CARBOHYD
                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                     the
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Q62179;
                                   DOMAIN
DOMAIN
                                                                                                                                           Pfam; PF01403; Sema; Pfam; PF01437; PSI; 1 SMART; SM00423; PSI;
                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     semaphorin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99253973; PubMed=10318831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pueschel A.W., Adams R.H., Betz H.;
"Murine semaphorin D/collapsin is a member
and creates domains inhibitory for axonal e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                 MGD; MGI:107559;
                                                                                                                                                                                                                                                                                                                 between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuron 14:941-948(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95267431; PubMed=7748561;
  CARBOHYD
                                                                                                                      Developmental
                                                                                                                                                                             InterPro; IPR002165; Plexin_repeat.
InterPro; IPR001627; Sema.
                                                                                                                                                                                                      InterPro; IPR003659; Plexin-like
                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH GIPC
                                                                                                                                                                                                                                                                                                                                                                                      Biol Chem. 274:14137-14146(1999).

FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDIS SPECIFY TERRITORIES INACCESSIBLE FOR GROWING A SUBUNIT: INTERACTS WITH GIPC PDZ DOMAIN.

SUBCELLULAR LOCATION: Type I membrane protein.

DEVELOPMENTAL STAGE: EXPRESSED FROM DAY 10 IN LEVELS FOUND BETWEEN DAYS 10-12, EXPRESSION PE MODERATE LEVELS FROM THEN UNTIL BIRTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDZ protein regulates the distribution of the transmembrane
                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLSKAV
                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L.-H., Kalb R.G.,
                                                                                                                                                                                                                              X85992; CAA59984.1; -.
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                                                                                                                                                                                                                    Sema4b
 662
683
782
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726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strittmatter S.M.;
                                                                                                                      Glycoprotein
                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL)
SEMA.
N-LINKED (GLCNAC. . N-LINKED (GLCNAC. .
                       BY SIMILARITY.
                                   PRO-RICH
                                                                                              EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleosto Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                               IG-LIKE C2-TYPE
                                                                                                                                domain; Multigene family; Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 782
                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                        ormatics and the EMBL outst There are no restrictions ong as its content is in
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sion.";
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(POTENTIAL).
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EMBL outstation •
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Best Local S
Matches 81
                                                                                                                                                                 NALL HUMAN STANDARD;
NALL HUMAN STANDARD;
NALL HUMAN STANDARD;
NALL HUMAN STANDARD;
O9COT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NACHT-, LRR- and PYD-containing protein 2 (Death effector filament-forming ced-4-like apoptosis protein) (Nucleotide-binding domain and caspase recruitment domain) (Caspase recruitment domain protein 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
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CARBOHYD
SEQUENCE
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CARBOHYD
CARBOHYD
                                                       proteins.
Cell Deat
                                                                                                                                                                                                                                                                                  HUMAN
                     SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=21148093; PubMed=11250163;
                                                                            Bertin J., DiStefa
                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=21169419; PubMed=11270363;
                                                                                                                                             Mammalia;
                                                                                                                                                         Eukaryota;
 Martinon F., Hofmann
"The pyrin domain: a
                                                                                                                                   NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                              714
                                                                                                                                                                                                                                                                                                                                                    381
                                                                                                                                                                                                                                                                                                                                                                          675
                                                                                                                                                                                                                                                                                                                                                                                                324
                                                                                                                                                                                                                                                                                                                                                                                                                      615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L-LCRRLLSPMNLLSLHTASGLRLFS-~---VLSLAWGFIADVDLESEKYRRLGEMRFTL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAVT-LSSRVHIIEELQIFPQGQPVQNLLLDSHGGLLYASSH-SGVVQVP----VANCSL
                                                                                                                                                                                                                                                                                                                                                    EEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVLNFLKDH----FLMDGQVRSRLLLLLQPRARYQRVAVHRVPGLHSTYDVLFLGTGDGRLH 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELG - - - RWDALVVMSGDGLMH
                                                                                                                                                                                                                                                                                                                                                                          VLLFLFFLYRHRDGMKLFLKQGE
                                                                                                                                                                                                                                                                                                                                                                                               VVAFRL---EPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPQQMPPP
                                                                                                                                                                                                                                                                                                                                                                                                                      YCPEVMEEGVMDQKNQRDGTPVIINTSRVSAPAGGRDSWGADKSYWNEFLVMCTLFVFAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APVNASASCRVLPTGDLLLV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----ELCKNSSYKAR--FLVPGK-----PCKQVQIQPNTVNTLACPLLSNLATRLWVHNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSH-WT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YPTCGDCLLARDPYCAWTGSACRLASLYQPDLASRPW--TQDIEGASVK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVVNGLMERPDWETAIQ----
                                                        Death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81; Conservative
                                                                                                                                             Eutheria;
                                                                                                                                                                                                                                                                                                                                                     384
                                                                         Distefano P.S.; domain: a novel motif found
                                                                                                                                                          Metazoa;
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88
356
471
526
574
639
782 7
                                                        Differ.
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356
471
471
526
639
639
                                                                                                             (ISOFORM
                                                        7:1273-1274(2000)
                                                                                                                                             Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.6%;
19.1%;
                                                                                                                                                         Chordata;
K., Tschopp J.;
possible member
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X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 92; DB
Pred. No. 4.1;
19; Mismatches
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                                                                                                                                                          Craniata;
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  of
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(GLCNAC.
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  the death
                                                                             apoptosis
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                                                                                                                                                                                                                                                                                                                                                                           -CASVHPKTRPIVLPPE
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  domain-fold
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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  family
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C: SUBUNIT: Interacts strongly with caspase 2, weakly with caspase 9
c and with APAP1 in a cytochrome c-inducible way leading to the
c formation of an apoptosome. This interaction may be ATP-dependent.
C: SUBCELLULAR LOCATION: Cytoplasmic.
C: ALTERNATIVE PRODUCTS: 4 isoforms; I/NAC beta/DEFCAP-L (shown here), 2/NAC alpha/DEFCAP-S, 3/NAC gamma and 4/NAC delta; are
c produced by alternative splicing.
C: TISSUE SPECIFICITY: Widely expressed. Isoforms 1 and 2 are
expressed in peripheral blood leukocytes, chronic myelogenous
c leukemia cell line K-562, followed by thymus, spleen and heart.
C also detected in lung, placenta, small intestine, colon, kidney,
C ilver and muscie.
C: SIMILARITY: CONTAINS 1 NACHT DOMAIN.
C: SIMILARITY: CONTAINS 1 CARD DOMAIN.
C: SIMILARITY: CONTAINS 7 LEDCINE-RICH REPEATS (LRR).
EMBL; AF298548; AAG15254.1; -.
EMBL; AF310105; AAG30288.1; -.
EMBL; AF229059; AAK00748.1; -.
EMBL; AF229060; AAK00749.1; -.
EMBL; AF229061; AAK00750.1; -.
EMBL; AF229062; AAK00751.1; -.
EMBL; AF229062; BAA760770.1; -.
EMBL; AB23143; BAA76770.1; -.
                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemsubmitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Ishkawa K.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 6:63-70(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A novel enhancer of the Apafl apoptosome involved in cytochrome c-dependent caspase activation and apoptosis.";
J. Biol. Chem. 276:9239-9245(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21153743; PubMed=11076957;
Hlaing T., Guo R.-F., Dilley K.A., Loussia J.M., Morrish T.A.,
Shi M.M., Vincenz C., Ward P.A.;
                                                                                                                                                                      or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chu Z.-L., Pio F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and characterization of DEFCAP-L and -S, two soforms of a novel member of the mammalian Ced-4 family of apoptosis proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        implicated
Curr. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Uterus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSSUE-Erythroleukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 276:9230-9238(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activation of pro-caspase-9 and consecutive apoptosis Seems to bind ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nitted (SEP-1999) to the EMBL/GenBank/DDBJ dirabases. FUNCTION: Able to form cytoplasmic structures termed death effector filaments. Enhances APAF1 and cytochrome c-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in apoptosis and inflammation."; 11:R118-R120(2001).
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Matches 89
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CONFLICT
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0364; DISEASERSIST.
SMART: SM0368 LRR_RI: 5.
PROSITE; PS50209; CARD: 1.
PROSITE; PS50824; DAPIN: 1.
PROSITE; PS50824; NACHT: 1.
Apoptosis; ATP-binding; Leucin
1126 EIEFCVWDQFLGEINPQHSWMVAG 1149
                                           1091
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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MIM; 606636; -.
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InterPro; IPR001611; LRR.
                                                                                                             242
                                                                                                                                                                                                                                                                   815
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                    DGELMVSEAVQGQVHPNYFWMVSG
                                                                 HLFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDG-----KGVFAV 340
                                                                                      PIAEIAEESSPE---VVPVE----LLCVPSPASQGDLHTKPLGTDDDFWGPTGPVATEV- 1090
                                                                                                                                 SRRKPSVMTPTEGLDTGEMSNSTSSLKRQRLGSERAASHV
                                                                                                                                                      -----AYLPVGRVGSKTPASPVVVQQGPVDAHLVPL----
                                                                                                                                                                            KELDLQQNNLDDVGVRLLCEGLRHPACKLIRLGLDQTTLSDEMRQELRALEQEKPQLLIF
                                                                                                                                                                                                  ADVDLESE----
                                                                                                                                                                                                                        TLTELDLSFNVLTDAGAKHLCORLROPSCKLQRLQLVSCGLTSDCCQDLASVLS-ASPSL 924
                                                                                                                                                                                                                                             QVTNEDLLTNC-----TLLLCRRLLSP------MNLLSLHTASGL--RLFSVLSLAWGFI 174
                                                                                                                                                                                                                                                                   LSGNSLSHSAVKSLCK----TLRRPRCLLETLRLAGCGLTAEDCKDLAFGLR---ANQ 865
                                                                                                                                                                                                                                                                                        MSGDGLMHEVVNGLMERPDWETAIOKPLCSLP----AGSG-----NALAASLNHYAGYE 127
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                          --EEPVPSHWTVVPDEDFVLVLAL------LHSH-LGS-EMFAAPMGRCAAGVM 285
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                                           -- VDKEKNL----YRVHFPVAGSYRWPNTGLCFVMREAVTV 1125
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                                                                                                                                                                                                                                                                                                              42; Mismatches
                                                                                                                                                                                                  ----KYRRLGEMRFTLGTFLR--LAALRTYRGRL---
                                                                                                                                                                                                                                                                                                                                                           Μ¥.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).

MISSING (IN ISOFORM 3

MISSING (IN ISOFORM 2

K->L: NO EFFECT.

K->S: NO EFFECT.
                                                                                                                                                                                                                                                                                                                        Score 92; Pred. No. 9
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LRR 2.
LRR 3.
LRR 4.
LRR 5.
LRR 6.
LRR 7.
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Y S (IN REF. )
Y M (IN REF. )
Y I (IN REF. )
Y V (IN REF. )
Y V (IN REF. )
Y C (IN REF. )
                                                                                                                                                                                                                                                                                                                                                        438F0DCE45C2562D CRC64;
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2 AND ISOFORM
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RESULT 14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT DEGRADATION OF UBIQUITINATED PROTEINS. THE REGULATORY (OR A COMPLEX CONFERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO 26S COMPLEX (BY SIMILARITY).
008651;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00382; AAA; 1.
TIGRFAMS; TIGR01242; 265p45; 1.
PROSITE: PS00574; AAA; 1.
Hypothetical protein; Proteasome; ATP-binding; Nuclear protein.
NP_BIND 202 209 ATP (POTENTIAL).
NP_BIND 202 209 ATP (POTENTIAL).
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Rhabditidae; Pel
NCBI_TaxID=6239;
                          SERA_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Du
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01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Bristol N2;
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15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003960; AAA_sub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003959; AAA_ATPase_centr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WormPep; F23F12.6; CE01253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U12965; AAA20608.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities
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                                                                                                                          205 TYRGRLAYLPVG-----RVGSKTPAS
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                                                                                                PPRGVLMYGPPGCGKTMLAKAVAANTAAS
                                                                                                                                                     ALVDVLPPEADSSIQMLRPDEKPDISYGDIGGLDMQKQEVREAVELPLTHGELYQQIGID 193
                                                                                                                                                                                    RLFSVL--
                                                                                                                                                                                                             -KRIQSVPLVIGQFLEAVDQNHAIVGSTTGSNYYVRVLSILDRELLKPGCSVALHKYSN-
                                                                                                                                                                                                                                      QKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGL
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                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                   414 AA;
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(Rel. 32,
(Rel. 36,
(Rel.
                                                                                                                                                                                                                                                                                                                             Conservative
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                            STANDARD;
36, Created)
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                                                                                                                                                                                                                                                                                                                                                                                   46358 MW;
                                                                                                                                                                                                                                                                                                                                        4.48; 22.08;
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                                                                                                                                                                                ---SLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALR
                                                                                                                                                                                                                                                                                                                            27;
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                                                                                                                                                                                                                                                                                                                                        Score 89;
Pred. No.
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                            PRT;
                                                                                                                                                                                                                                                                                                                         core 89; DB 1; red. No. 3.2; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                   8630AFFB8A2C7F32 CRC64;
                                                                                                222
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RESULT 15
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Best Local
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ACT_SITE
ACT_SITE
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PROSITE; PS00670; D_2_HYDROXYACID_DH_2; 1.
PROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.
Serine biosynthesis; Oxidoreductase; NAD.
ACT_SITE 236 236 SUBSTRATE-BIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; p.08328; 1PSD.
InterPro; IPRO02162; D_2hydac_dh.
Pfam; pF00389; 2-Hacid_DH; 1.
Pfam; PF02826; 2-Hacid_DH_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institute modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X97772; CAA66374.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Serine biosyl-!- SUBUNIT: Homotetramer
-!- TISSUE SPECIFICITY: L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: 3-phosphoglycerate + NAD(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning, sequencing and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Achouri Y., Rider
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEHYDROGENASES FAMILY.
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                                                                                                                                                                                      FVLV-LALLHSHLG---SEMFAAPMGRCAAGVMHLFYVRAG-VSRAMLLRLFLAMEKGR 310
                                                                                                                                                                                                                                                                                                   VGSKTPA---
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                                                                                                                                   FITVHTPLLPSTTGLLNDSTFA-
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283
533 AA;
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M.H., van Schaftingen E., Robbi M.;
M.H., van Schaftingen E., Robbi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236
265
283
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Pred. No. 4.5;
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BY SIMILARITY
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SERA_HUMAN

STANDARD;

PRT;

533

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EMBL; AF006043; AAB88664.1; ...
EMBL; AF171237; AAD51415.1; ...
EMBL; BC000303; AAH00303.1; -..
EMBL; BC0011349; AAH01349.1; -..
EMBL; BC011262; AAH11262.1; ...
HSSP; POB328; IPSD,
Genew; HGNC.8923; PHGDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
I- CATALYTIC ACTIVITY: 3-phosphoglycerate + NAD(+) = 3-phosphohydroxypyruvate + NADH.
I- Phosphohydroxypyruvate + NADH.
I- PATHMAY: Serine blosynthesis; first step.
I- SUBUNIT: Homotetramer (By similarity).
I- DISEASE: Defects in PHGDH are the cause of a deficiency.
I- DISEASE: Defects in PHGDH are the cause of a deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        043175; Q9BQ01;
15-JUL-1999 (Rel. 38, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (3-PGDH).
                                                                                                         PROSITE; PS00065; D_2_HYDROXYACID_DH_1; 1.
PROSITE; PS00670; D_2_HYDROXYACID_DH_2; 1.
PROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.
Setine blosynthesis; Oxidoreductase; NAD; D
ACT_SITE
236
236
236
                                                                                                                                                                                                        InterPro; IPR002162; D_2hydac_dh.
Pfam; PF00369; 2-Hacid_DH; 1.
Pfam; PF02826; 2-Hacid_DH_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klomp L.W.J., de Koning T.J., Malingre H.E.M., van Beurden E.A.C.M., Brink M., Opdam F.L., Duran M., Jaeken J., Pineda M., van Maldergem L., Poll-The B.T., van den Berg T.E.T., Berger R., "Molecular characterization of 3-phosphoglycerate dehydrogenase deficiency - a neurometabolic disorder associated with reduced L-serine blosynthesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-20179699; PubMed-10713460;

Cho H.M., Jun D.Y., Bae M.A., Ahn J.D., Kim Y.H.;

"Nucleotide sequence and differential expression of the human 3-phosphoglycerate dehydrogenase gene.";

Gene 245:193-201(2000).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                 VARIANT
                                                                                                                                                                                                                                                                      MIM; 601815
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                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain, Lung, and Muscle;
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SIMILARITY: P
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                                                 Juctase: NAD: Disease mutation.
SUBSTRATE-BINDING (BY SIMILARITY).
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V -> M (IN PHGDH DEFICIENCY).
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V -> M (IN PHGDH DEFICIENCY)
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                                                                            202 FITVHTPLLPSTTGLLNDNTFA----QCKKGVRVVNCARGGIVDEGALLR---ALQSGQ 253
                                                                                                                                                                                             218 VGSKTPA-----SPVV-----VQQGPVDAHLVPLEEPVPSHWTVVPDED 25
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                                                                                                                                                                                                                                                                                                                                                                                                                             51 LMLTERRNHARELYRSEELGRWDALYYMSGDGLMHEVVNGL------MERPDWE 98
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                                                                                                                                                                                                                                      S-----NGKTLG1LGLGR 155
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533 AA;
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C.Species: Arabidopsis thaliana (r C:Date: 23-Apr-1999 #sequence_revi C:Accession: T05162 R:Bevan, M.; Peters, S.A.; van Sta submitted to the Protein Sequence A:Reference number: 215400 A:Accession: T05162 A; Map position: 4 A; Introns: 44/3; 1 A; Note: F18E5.160 A;Molecule type: DNA A;Residues: 1-1240 <BEV> A;Cross-references: EMBL.ALO22603 A;Experimental source: cultivar Columbia; BAC clone 20 밁 δÃ DЬ δõ 밁 Qy 밁 δÃ Ď, δÃ 밁 C; Genetics: Best Local Similarity Matches, 122; Conserv Query Match 374 LGRPKRLLVEVNPEGGKKSAREIFVKEVKPLFEDADVQLEIQETKYQLHAKEFVKSMDVS 433 191 11 LPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELG 70 PHVSDKEVGYQGPETKFEDLEWREMKGPFVTIW-----EP----KDGKGVFAVDGELM 345 APAAKFSDGYLDLIVLK-NCPKLVLLSLMRQTSSGTHV--ESPYIVYIKLTVEKVKAFVL 710 APMGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYV-----PVVAFRL 329 RIDFYVCLVDKFUNYCIAVVKLLALQRIICLRRYNGRILFLPAPGFEGYGQPASCSLYQE 607 RFTLGTFL-----NEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEM 190 ·····QGP----VDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHS-HLGSE-MFA Conservative 117/3; 178/3; 206/1; 237/2; 375/1; 416/1; 449/3; 474/1; 503/1; 529/1 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999 22.4%; Score 451; DB 2; Length 1240; 31.9%; Pred. No. 1e-31; Sequence Database, August 1998 van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, 63; Mismatches 127; -----LHNVPWGSENTLT F18E5 Indels 70; Gaps 230 653 13;

EPGALVDEPDKEGIIDSDGEVL 732

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hypothetical protein C34C6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: C5-Caenorhabditis elegans
C;Accession: T19707
R;Percy C
                              hypothetical protein YLR260w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L8479.7
C.Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revisian 12-May-1995 #text_change 19-Apr-2002
C:Accession: S51398
R;Miller, N.
submitted to the BBL Data Library, November 1994
A.Description: The sequence of S. cerevisiae cosmid 8479.
A:Reference number: S51395
A:Reference number: S51395
A:Accession: S51398
A:Molecule type: DNA
A:Residues: 1-687 <MIL>
A:Gonetics: L901-C081; MIPS:YLR260W
A:Gross-references: SGD:S0004250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 KYRR-LGEMRFTLGTFLRLAALRTYRGRLAYLP-----VGRVGSKTPASPV--- 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 KYGTKMNEKSVMERALEIATSPTAKAESVALYSVKTDNQSYASFLSIGWGLMADIDIDSE 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 GYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHT--ASGLRLFSVLSLAWGFIADVDLESE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 KADLGKFNGVLILSGDGLVFEALNGILCREDAFRIFPTLPIGIVPSGSGNGLLCSV--LS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 SEELGRWDALVVMSGDGLMHEVVNGLMERPD-WETAIQKPLCSLPAGSGNALAASLNHYA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 PPPQEQCRGNLLVFINPNSGTGKSLETFANTVGPKLDKSLIRYEVVVTTGPNHARNVLMT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 PRP---CR--VLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARE-LVR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 18.6%; Score 374.5; DB 2; Local Similarity 28.6%; Pred. No. 1.9e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -VVQQGPVDAHLVPLEEPVPSHW------TVVPDEDFVLVLALLHSHL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110;
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                                                                      190 MRFTLGTFLRL-------AALRT-----YRGRLAYLPVGRVGSKTPASPVVV 229
271 NRAYLGFFLRLFQKPDWKCSIEMDVVSSDRTEIKHMYEKSKNLAPM----SESSDSDKTV 326
                                                                                                                                                 216 -KPALTALEILKGR-----PTSFDLMTFEQKGKKAYSFLTANYGIIADCDIGTENWRFMGE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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hypothetical protein SPAC4AB.07c - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T38776 R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V, submitted to the EMBL Data Library, August 1997
                                                                                                                                                                             A;Reference number: Z21751
A;Accession: T38776
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:298762; PIDN:CAB11477.1; GSPDB:GN00066; SPDB:SPAC4A8.07c
A;Experimental source: strain 972h-; cosmid c4A8
                                                                                            A; Molecule type: DNA
A; Residues: 1-458 < SKE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         621 KGSHVLQ--PEVLHSKILAYKIIPKLGNGLFSVDGEKFPLEPLQVEIMP 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 KGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHP 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562 L-DPNISNNLGIFYTGKMPYVAADTKFFPAALPSDGTMDMVITDARTSLTRMAPILLGLD 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 ELGVAFNIIQKKKYPCEIYVKYAAKSKNELKNHYLEHKNKGSLEFQH1TMNKDNEDCDNY 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 TLGTFLRLAALRTY------ 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 INCTLLLCRRLLSPMNLLSLHTASGLR---LFSVLSLAWGFIADVDLESEKYRRLGEMRF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 CASGDGIPHEVINGLYQRPDHVKAFNNIAITEIPCGSGNAMSVSC-HW-----TNNP-- 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 IFVIINPFGGKGKAKKLFMTKAKPLLLASRCSIEVVYTKYPGHAIEIAREMDIDKYDTIA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 VPDEDFVLVLALLHS----HLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAME 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               502 NYENEYETENEDEDEDADADDEDSHLISRDLADSSADQIKEEDFKIKYPLDEG1PSDWER 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 ---GRVGSKTPASPVVVQQGPVDAHLV--------PLEEPVPSHWTV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 SYSTLCLIKSIETRIDLMCCSQPSYAREHPKLSFLSQTYGLIAETDINTEFIRWMGPARF 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76; Mismatches 150; Indels 81;
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A; Map position: 1 A; Introns: 39/1; 101/1 ;Gene: SPDB:SPAC4A8.07c 162 SYDGILSVGGDGLFHEVINGLGERDDYLEAFKLPVCMIPGGSGNAFS----YNATGQL- 215 102 IKRSRRFIVFINPHGGKGKAKHIWESEAEPVFSSAHSICEVVLTRRKDHAKSIAKNLDVG 161 131 NEDLLTNCTLLLCRRLLSPMNL-LSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGE 189 71 RWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVT 130 109; Similarity Conservative 17.6%; Score 355; DB 2; Length 458; 29.5%; Pred. No. 1e-23; tive 64; Mismatches 144; Indels 12;

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hypothetical protein T10B11.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change C;Accession: T33517 R;Minx, P.; Kemp, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-624 <BOR>
A;Cross-references: EMBL:Z75078; NID:g1420415; PID:g1420417; GSPDB:GN00015; MIPS:YOR171d
                                                                               RESULT
T33517
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R;Bordonne, R.; Camasses, submitted to the Protein:
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N;Alternate names: hypothetical protein O3615
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
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Best Local
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                                                                                                                                          ILAYKIIPKVESGLFSVDGEKFPLEPLQVEIMP 604
                                                                                                                                                                                                                                                                                                SPVVVQQGPVDAHL
                                                                                                                                                                                                                                                                                                                               NLGVAFNIIQGKKYPCEVFVKYAAKSKKELKVHFLENKDKNKGCLTFEP-----NPSPNS
                                                                                                                                                                                                                                                                                                                                                            TLG-----RGRLAYLPVGRVGSKTP-A 224
                                                                                                                                                                                                                                                                                                                                                                                         SYAALCLVKSIETRIDLMCCSOPSYMNEWPRLSFLSQTYGVIAESDINTEFIRWMGPVRF 399
                                                                                                                                                                                                                                                                                                                                                                                                                       TNCTLLLCRRLLSPMNLLSLHTASGLR---LFSVLSLAWGFIADVDLESEKYRRLGEMRF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CASGDGIPYEVINGLYRRPDRVDAFNKLAVTQLPCGSGNAMSISC-HW-----TNNP-- 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VMSGDGLMHEVVNGLMERPDWETAIQK-PLCSLPAGSGNALAASLNHYAGYEQVTNEDLL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILVIINPHGGKGTAKNLFLTKARPILVESGCKIETAYTKYARHAIDIAKDLDISKYDTIA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPFECRVAP 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEP-KDGK-GVFAVDGELMVS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STSP-ESHLLTFE
                                                                                                                                                                       VVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHP 356
                                                                                                                                                                                                      KMPYIAKDTKFFPAALPADGTIDLVITDARIPVTRMTPILLSLDKGSHVLE--PEVIHSK 571
                                                                                                                                                                                                                                 ---HLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVP 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFY
                                                                                                                                                                                                                                                                SPDLLSKNNINNSTKDELSPNFLNEDNFKLKYPMTEPVPRDWEKM-DSELTDNLTIFYTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , A.; Madania, A.;
Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%;
25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 345; DB 2;
Pred. No. 1.2e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                               -VPLEEPVPSHWTVVPDEDFVLVLALLHS- 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martin, R.P.; Poch, O.; Tarassov, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                 29-Oct-1999
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                                                                                                                                                                                                                                                                                                                             454
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                 C; Genetics:
                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-306 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 1
A; Introns: 26/1; 76/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
 A; Gene: lin2702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CESP:T10B11.2
                                                                                                                                                                                                                                                                                                                                                                          AAMVKP 533
                                                                                                                                                                                                                                                                                                                                                                                                         SGCVEP 368
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submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid T10B11.
A;Reference number: Z2133
A;Accession: T33517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain Bristol N2; clone T10Bl1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AF098993; PIDN:AAC67466.1; GSPDB:GN00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-549 <MIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 RRVKNRPKNIIIFINPFGGNGKAQKIFKDNVDAFFWLTPGLRYKVVLTERANHARDYIVE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 RGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLL-AEAEISFTLMLTERRNHARELVRS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGNALAASLNHYAGYEQVTNED---
LYELDPSLNCYRVTKWSYQPDADQEDPGVWNLDGEILEQPKDEPLHFKLHPQLISFFGRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPPEQWSAIDGLVSVGGDGLFNELLSGALLRTQTDAGRNIDNPSSHLVTPHIRFGIIGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEYECPYLVYVPVVAFRLEP - - - KDGKGVFAVDGELM - - - VSEAVQGQVHP - - - NYFWMV
                                                                                                                                                                  PDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYV-RAGVSRAMLLRLFLAMEKGRH
                                                                                                                                                                                                                                                                                                                                                                                         FSVLSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRT-----YRGRLAYLPVGR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                SANSIVSTVHE-----TNDHATSAVHIAIGSECNVDVC-----TVHQHQKLIR
                                                                                                                                                                                                                                                                             VGSKTPASPVVVQQGPVDAHLVPLEEPVP-----SHW------
                                                                                                                                                                                                                                                                                                                                    ISANATSYGWLGDVLRDSEEYRCLGPIRY-----QWSALRTTIRHPIYRGMVQF----S 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109/3; 159/1; 187/3; 229/3; 353/1; 398/2; 434/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.4%; Score 250.5; 23.7%; Pred. No. 3e-
                                                                                                                                                                                                                      -KDQLPPCLEPCPVCMKPQGNDKYDYHWHAEFTHVICCVIPTVT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71;
                                                                                                           APFTGIGDGTLDLALVPRISRFHNMQFMRKVAMYGGKQ 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LLTNCTLLLCRRLLSPMNLLSLHTASGLRL 163
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AHIT769
Conserved hypothetical protein lin2702 [imported] - Listeria innocua (strain Clip1126 C)Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Date: 27-Nov-2001
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,
C; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A;Title: Comparative genomics of Listeria species.
A;Accession: AH1769
A;Accession: AH1769
A;Accession: AH1769
A;Accession: AH1769
A;Residues: 1-306 <GLA>
A;Residues: 1-306 <GLA>
A;Residues: 1-306 <GLA>
A;Residues: Strain Clip11262
C;Genetlcs:
A;Genetlcs:
A;Genetlcs:

Qy 191 RPTLGTELRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGDVDAHLVPLEEPVPSHWT 250	Query Match 7.0%; Score 140.5; DB 2; Length 306; Best Local Similarity 21.7%; Pred. No. 9.2e-05; Matches 76; Conservative 60; Mismatches 132; Indels 83; Gaps 16; Qy 16 RVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWD 73; Li	Qy 74 ALVWSCDGLMHEVVNGLMCRPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVT 130 Db 62 VYIAAGGDGTVNEVVNGLMCVEKRPKIGILPVGTTNDYARALNF 105 Qy 131 NEDLLTNCTLLLCRLLSPMNILSLHTASGLRLFSVLSLAMGFIADVDLESEKYRRLGEM 190 Db 106 AKDPLEALOIIAKGETIRVDIGKNETEFF-IN-MR- : : : : : : : : : : : : : : : : : :	Ouery Match 7.7%; Score 155.5; DB 2; Length 306; Best Local Similarity 22.2%; Pred. No. 4.2e-06; Matches 77; Conservative 66; Mismatches 129; Indels 75; Gaps 16; Matches 77; Conservative 66; Mismatches 129; Indels 75; Gaps 16; Oy 16 RVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARBLVRSEELGRWD 73 16 :::
RESULT 10 A83894 hypothetical protein BH1953 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans	. 112 116 196 165 251 210 309	RESULT 9 Hig995 hypothetical protein ytlk - Bacillus subtilis C;Species: Bacillus subtilis R;Species:	Oy 251 VVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLELAM 306

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ist, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber ist, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Carter, N.M.; hrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, e 300, 249-256, 1997

hors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. er, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino hors: 'Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau J.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete er, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlinors: Schleich, S.; Schroetter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sehi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya inters, P.; Mipat, A.; Yamamoto, H.; Yamano, K.; Yata, K.; Yoshida hors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

le: The complete genome sequence of the Gram-positive bacterium Bacillus subtili ereace number: A69580; MUID:98044033; PMID:9384377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oal protein ytlR - Bacillus subtills
: Bacillus subtills
5-Dec-1997 *sequence_revision 05-Dec-1997 *text_change 15-Oct-1999
                                                                                        GRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELM 345
                                                                                                                                                                                                  AVVSN-----HPFYGGGMKAAPLANPREKTEDIVIVE---NQPELKKYWLLCLMAF 257
                                                                                                                                                                                                                                                                                                                                                                                                     RVFLFLRL-----RFLVYPLSHLHASATFKPFTLACTTED-----ETREFHDVWF 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QE----IKKVKRPLT-RTFHLGS-VNFLQDKSQILYFMNHIGIGFDAYVNKKAMEFPLR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEMRFTLG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ≥ferences: GB:299119; GB:AL009126; NID:g2635411; PIDN:CAB14972.1; PID:e11858
≥ntal source: strain 168
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GKHTKMDGVTMFKAKDITF--YTKD-KIPFHADGEIM 291
                                                                                                                                                                                                                                                                                                 VVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFL--AMEK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---TELRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSH--WT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVIGGDGTMHEVVNGLKDVDDIE-----LSFVPAGAYNDFSRGFS-----IKKIDLI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVMSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASLNHYAGYEOVTNEDLL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11NPTAGHRNGLRVWKS-IQKELIKRKVEHRSFLTEHPGHAEVLARQISTIQEY-KLKRL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRS----EELGRWDAL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; nucleic acid sequence not shown; translation not shown
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1-309 <KUN>
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79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 136.5; DB 2; Length 309; 23.4%; Pred. No. 0.00021; ative 47; Mismatches 148; Indels 63
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R;Knnst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G; Azevedo, V.; Berter G; Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997.

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, V.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serori akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Althors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-postitive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
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R;Takami, H; Nukasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Tittle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A83894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved hypothetical protein yerQ - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-295 <STO>
                             A;Cross-references: GB:Z99107; GB:AL009126; NID:g2632866; PIDN:CAB12492.1; PID:e1182652
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δõ
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                                                                                     A; Residues:
                                                                                                             A; Molecule type: DNA
                                                                                                                                       A; Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 TLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADV--DLESEKYRR-----LGEM 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 VLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRWDALVVM 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LIVNKASGNGKGQRTWKK-VEYELQIRNTPYLVRFTSGSGHATTIVKELLTEGVKTIIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVPDEDF----VLVLALLHS-HLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAM 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGDGTINEVANGLVNH-----RVPLGIIPAGSGNDFARCLNIPMHYEKALHR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLTNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YKGKHVVMEQHVTLLTGKDVYV-----QSDTPVLVQSDGEPIMESPVRLQI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKGRH--MEYECPYL----VYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQV 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDGKELFFSGVWLVAVANSPNYGGGIRICPEASYDDGLLNICVVH-GMSKWQLLRLFPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYVLS---MLEVLKDYR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---IFENKQKKVDLLHLGQRHCLTVTGI-----GFDGKIAKTVNEAIYKNWFNQFGFGGL 161
                                                                                  1-303 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No. 0.00076;
                                                                                                                                       sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 295
                                                                                                                                          translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PTNIQIT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88;
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175
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A;Title: The complete genome sequence of the lactic acid A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: D86677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403) c;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: D86677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE005176; PID:g12723295; PIDN:AAK04518.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-342 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.3%; Score 127; DB 2; Best Local Similarity 20.4%; Pred. No. 0.0017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184
                                                                                                                                                             191
                                                  237 HLVPLEEPVPSHWTVVPDE-----DFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVR 291
                                                                                                                                                                                                                                                                     131
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                                                                                                                                                                                                                                                                                                                           61
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les 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yecE
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                                                                                                                                                                                                                                                                NEDILTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEM 190
                                                                                                                                                                                                                                                                                                                           LIIAAGGDGTINEVVAGISPFEKRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLLNPRGGKGKALQLERSHVQPLLAEA----EISFTLMLTERRNHARELVRSEELGRWD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRCAAGVMHLFY----VRAGVSRAMLLRL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVTLTNSVGGFEKLAPDSSLNDGMFDLMILKKANLAEFIRVATMALRGEHINDQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNEDLLTNCTLLLCRRLLSPMNL------LSLHTASGLRLFSVLSLAWGFIADVDLESEK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DALVVMSGDGLMHEVVNGLM---ERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVLVLLNPRGGKGKALQLFRSHVQPLL---AEAEISFTLMLTERRNHARELVRSEELGRW 72
                                                                                                                                                                                                                                                                                                                                                                              ALVVMSGDGLMHEVVNGLM---ERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                   LIYNPTSGQ----EIIKKYIADILDKLEQYGYEASAYQTTAEQDSAKKEAARATEAG-FD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVPLEEPVPSHWTVVPDEDF - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PREDILKAADTVI-NGVARPIDIGQVNGQYFINIAGGGRLTEL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RARIIYNPTSGR----EIFKKHLAQVLQKFEQAGYETSTHATTCAGDATHAAKEAALREF
ELLPRVRKAPVR--VVHDEGVFEGDISMFFAALTNSVGGFEKIAPDAKLDDGLFTLILVK 232
                                                                                                     ----FINTAAGGGLTELTYSVPSHLKTAFGYLAYLAKG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----HIIYTKANRVKVNVSEKMQLNL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                   ----KPLEAIEI----IGKNQILNIDVGHAVIRETQDEQY---
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20.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55; Mismatches 122;
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Pred. No. 0.00087;
                                                                                                                                                             ---LRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDA 236
                                                                                                                                                                                                                                                                                                                        ---LAIVPTGTTNDFARALKIPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -VLVLALLHSHLGSEMFAAPM 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----QGEIMLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TYDVPSKL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K.; Weissenbach,
                                                                                                        ----A 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus
                                                                                                                                                                                                                   --- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   6.Q
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D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Meok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Scatcus: preliminary

A:Molecule type: DNA

A:Residues: 1-310 GCIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein homolog lin1865 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua (c;Species: Listeria innocua (c;Date: 27-Nov-2001 *sequence_revision 27-Nov-2001 *text_change 27-Nov-2001 C;Accession: Ac1665 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker R;Glaser, P.; Frangeul, L.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
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Genome Res. 11, 731-753, 2001
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A;Experimental source: strain IL1403
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A; Residues: 1-302 <STO>
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A;Cross-references: GB:AL592022; PIDN:CAC97095.1; PID:g16414366; GSPDB:GN00178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 PSVLRGMHLKH------PLFLHRVSPQ-----FSV--ELAESQPVOIDGEIH 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 ---QEISLENAFLMTFTKHPYFGGGVKISPEATNENADIHL----VEYNKHHLLRTFSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 -AMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQ--GQVH 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 SHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLEYVRAGVSRAMLLRLFL-- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 QVLNKLKLGSF-----SYI-----LTALHVLITKKPFPA-LIEVEN--- 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 EM--RFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 INHEIFIMN------YOSKGLSGYALNNIGIGLDATI-VKSANEGKLK 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 VLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRS--EELGRWDALV 76
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1 Similarity 21.2%; Pred. No. 0.0018;
75; Conservative 64; Mismatches 123; Indels
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Job time : 26 secs
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multidrug resistance protein bmrU [imported] - Bacillus halodurans (strain C-125) c;Species: Bacillus halodurans (c;Species: Bacillus halodurans c;Date: 01-Dec-2000 *sequence_revision 01-Dec-2000 *text_change 15-Jun-2001 c;Date: 01-Dec-2000 *sequence_revision 01-Dec-2000 *text_change 15-Jun-2001 c;Accession: F83871
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C:Genetics:
A:Gene: lin1865
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A; Molecule type: DNA
A; Molecules: 1-311 <STO>
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83871
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A;Experimental source: strain C-125
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 AMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGEL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 ....-VFEGEVMFFLLGLTNSIGGFEKI-APDAKLDDGKFSLIIVKK-VNL 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 -RRLGEMRETLGTELRLAALRTYRGRLAY------LPVGRVGSKTPASPVVVQQGPVDA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 -----RALHVPRDV-----IKATKIIAAGQSVAMDIGKANDTYFINIGG 139
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60 IVMCGDGTVHECINGLAVSPS-----PPPLVVLPTGTCNDFARSL 99
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es 32; Conserv
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Maximum Match 100%
Listing First 45 summaries
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Pred. No.

is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                CTGCACGCTATTGCTGTGCCGGCGGCTGCTGTCACCCATGAACCTGCTGTCTCTGCACAC 599
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Nava.V.E., Lacana',E., Poulton,S., Liu,H., Sugiura,M., Kono,K.,
Milstlen,S., Kohama.T. and Spiegel.S.
Direct Submission
Submitted (23-FEB-2000) Biochemistry, Georgetown University, 3900
Reservoir RD NW BSB Rm 357, Washington, DC 20007, USA
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Pred. No. 7.1e-279; 
0; Mismatches 7; Indels 1;
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TITLE
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                                        GGTCGAGGTTATGGATCCAGCGGGCGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGCGT
                                                                                               AGCCGCCGCCACGGGCACACGCGCCACAGGGACCCCCTGGCAGCGGGAGCCGCG
GCTGGTGCTGCTGAACCCGCGCGGCGGCGAGGGCAAGGCCTTTGCAGCTCTTCCGGAGTCA
                                                                                                                                       GCCCCACAGCCGGCCCTGCGACGCCCCGCCTGGGCAGCACCGATAAGGAGCTGAAGGCAGG
                                                                                  AGCCGCCGCCACGGGCAGCCCCCCACAGCGCCCAGGGGACCCCCTGGCAGCGGGAGCCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.systemsbiology.org
contact: amadan@systemsbiology.org
anuo Madan, Rachel Dickhoff, Jessica Fahey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
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                                                                                                                                                                                                                                                                 354
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                    /product="Unknown (protein for MGC:15041)"
/protein_id="AAH8040.1"
/protein_id="AAH8040.1"
/db_xref=="GC:14145486"
/translation="MDPAGGPRGVLPRPCRVLVLNPRGGKGKALOLFRSHVQPLLAE
AEISFIMALTERNHARELVRSSELGRADALVVMSGDGLMHEVVMGLMERPDWETAIO
KPLCSLPAGSGNALAASLNHYAGYEDYTNEDLLTNCTILLCRELLSPHNLLSHTASE
LRLFSVLSLANGFIADVDLESEKYRRLGEMRFTLGTFILLAALRTYRGRLAYLPVGRV
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551 c 592 g 327 t
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MGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pOTB7" 339. .1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:15041 IMAGE:3831657"
/closue_type="Skin, melanotic me.
/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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99.4%;
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Primates;
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                                                                               CTACTTCTGGATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCCAGCAGAT
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                                                                                                                                                                                                                                                                Submitted (33-AuG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hi.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) REDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction. 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, interest of Tokyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Mishikawa,T., Nagqi,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiyuchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishil,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y., Nihomiya,K. and Iwayanagi,T., Napo, Dhuman, CDNA sequencing project
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oligo capping: fis (full insert sequence).
Homo sapiens Mammary gland cDNA to mRNA, clone_lib:MAMMAL
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1821 bp mRNA linear PRI (
Homo sapiens cDNA FLJ12340 fis, clone MAMMA1002268, moder
similar to Mus musculus sphingosine kinase (SPHK1a) mRNA.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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University of
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Direct Submission
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                                                                                      /organism "Homo sapiens"
/db_xref="taxon:9506"
/clone="MAMMA1002268"
/tissue_type="Mammary gland"
/clone_lib="MAMMA1"
/note="elloning vector: pME18SF
393. 1547
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/prottein_id="BAB14028.1"
/db_xref="G1:10433791"
/translation="MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAE
                                                    /codon_start=1
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                                                                     /note="unnamed protein product"
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AEISFTLMLTERRNHARELVRSEELGRWDALLVNASGDGLMHEVVNGLMERPDWETAIO
RPLCSLPAGSGNALAASI.NHYAGY EGYTNEDLLTNGTLLLCRRLLSPANLLSLHTASG
LRLFSVLSLAMGF IADVDLESEKYRRLGEMRETLGFEPLRLAALRTY RRHLAXLFYGRV
GSKTPAS.PVVVQQGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLAILHSHLGSEMFAAP
MGRCAAGVHHLFYVRAGVSRAMLLRLFLAMEKGRHMEY ECPYLVYVPVVAGRRLEPRDG
KGVFANJOBELMVSEAVQGOVHPNYFWNVSGCVEPPPSWKPQQMPPPEEPL*
301 a 569 c 614 g 337 t

Matches 1558; 563 GAACCACGCGCGGAGCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGT 622 GAACCACGCGCGGGAGCTGGTGCGGTCGGAGGAGGTGGGCCGCTGGGACGCTCTGGTGGT 359 CGTGCAGCCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCG CGTGCAGCCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGGG GCTGGTGCTGAACCCGCGCGGGGGAAGGGCAAGGGCCTTGCAGCTCTTCCGGAGTCA GCTGGTGCTGCTGAACCCGCGCGGCGAAGGGCAAGGGCCTTGCAGCTCTTCCGGAGTCA 239 GGTCGAGGTTATGGATCCAGCGGGGGGGGGGCCCCCGGGGGCGTGCTGCCGCGT 442 GGTCGAGGTTATGGATCCAGCGGGCGGGGCCCCCGGGGGCGTGCCCGGGGCCCTGCCGGGT 179 AGCCGCCGCCACGCCCACACCCCCACAGCGCCCCTGGCAGCGGGAGCCGCG 382 ACCCGCCCCCAGGGCAGCG-CCCCACAGCGGCCAGGGACCCCCTGGCAGCGGAGCCGGG 119 CCTTGTGCCACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGACGACGACGT 899 AGTGGGTTCCAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCCGGTAGATGCACA 1102 AGTGGGTTCCAAGACACCTGCCTCCCCCGTTGTGCTCCAGCAGGGCCCGGTAGATGCACA AGCTTCCTTGAACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAA 539 Similarity Conservative 98.3**%**; 99.9**%**; 0; Score 1547; DB 9; Pred. No. 3.6e-278; 0; Mismatches 0; Length 1821; Indels 502 562 299 . 839 1042 982 922 659 862 802 479

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                                                                                 Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzu Mishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K. Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayar NEDO human CDNA sequencing project
                Direct Submission Submitted (23-AUG-2000)
                                                                                                                                                                                                                                                               oligo capping; fis (full insert Homo sapiens ovary, tumor tissue clone:OVARC1001809.
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mest Local Similarity Matches 1548; Conserv
                     CAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCTGTAGGAAGAGAGTGGGTTCCA 790
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CAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTCCA
                                                                                                  GTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTGG
                                                                                                                          GTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTGG 730
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1 (bases 1 to 1719)

Allen,J., Gosink,M., Melendez,A.J. and Takacs,L.

Human sphingosine kinase gene
Patent: WO 0131029-A 1 03-MAY-2001;

WARNER-LAMBERT COMPANY (US)

Location/Qualifiers
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/db_xref="taxon:9606"
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Pred. No. 1.1e-276;
^ wismatches 15;
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         1 (bases 1 to 1693)
Melendez,A.J., Carlos-Dias,E., Gosink,M., All
Human Sphingosine Kinase, Molecular Cloning,
Characterisation and Tissue Distribution
                                                                                           Homo sapiens sphingosine
AF266756
                                           Mammalia;
                                                 Eukaryota; Metazoa;
                                                         Homo sapiens
                                                                    Homo sapiens.
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                                          Eutheria;
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 press
                                          Chordata;
Primates;
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e kinase
                                         Craniata; Vertebrata; Catarrhini; Hominidae;
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                        Allen, J.M.
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TGCTGTGCCGCCGGCTGTCACCCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGGC
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Melendez,A.J., Carlos-Dias,E., Gosink,M., Allen,
Direct Submission
Submitted (11-MAY-2000) Department of Molecular
Biology, Jouveinal Parke-Davis, 11-13 rue de la
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/codon_statt=1
/rodon_statt=1
/product="sphingosine kinase"
/protein_id="AAF73470.1"
/protein_id="AAF73470.1"
/db_xref="GI:8133100"
/translation="MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALOLFRSHVQPLLAE
AEISFT_MATEERNHARELVRSSELGRWDALVVMSGDGLMHEVVNGLWERPDWETAIQ
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KPLCSLPAGSGNALAASLNHYAGYEQYTNEDLLTNCTLLLCRRLLSGMNLLSLHTASG
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GSKTPASPYVYQQGPYDAHLYPLEEPYPSHWTYVPDEDFYLVLALLHSHLGSEMFAAP
MGRCAAGYMHLFYYRAGYSRAMLLRLFLAMEKGRHMEYECPYLYYVPYVAFRLEPKDG
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/chromosome="17"
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270. .1424
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Pred. No. 1.9e-274;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                   Submitted (19-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                             Homo sapiens, clone MGC:15040
BC009419
BC009419.1 GI:14495624
                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
  NIH-MGC Project URL:
                                                        Direct Submission
                                                                   Strausberg,R.
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http://mgc.nci.nih.gov
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15040 IMAGE:3506924, mRNA,
                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                   through the I.M.A.G.E. Consortium/LLNL at: http://image.ll
Series: IRAL Plate: 23 Row: e Column: 1
This clone was selected for full length sequencing because
passed the following selection criteria: matched mRNA gi:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Rat Rutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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Tissue Procurement: DCTD/DTP
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/clone_lib="NIH_MGC_14"
/lab_host="DH10B-R"
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/translation="WpbyVQCGRGLFGEVFSAGGPRGYLPRPCRVLVLLNPRGGKGKA
LOLFRSHVOPLLAEAEISFTLMLTERRNHARELVRSEELGRWDALVVMSGDGLMHEVV
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1691 GGTGAGAAGGTGGAGGCTATGCTTTTGGGGGGACAGGCCAGAATGAAGTCCTTGGGTCAGGA 1750
                                                                         197 CGCGCGGCGGCAAGGGCAAGGCCTTTGCAGCTCTTCCGGAAGTCACGTGCAGCCCCTTTTGG 256
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team): 2-6-7 Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team): 2-6-7 Kazüsa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library Research Association for Biotechnology CDNA Library Research Association for Ministrute (HRI) (supported by Japan Key Technology Center etc.); 5-6 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AK095578.1 GI:21754862 oligo capping; fis (full insert sequence). Homo sapiens fetal brain cDNA to mRNA, clone_lib:FCBBF3 clone:FCBBF3001302.
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Isogai, T. and Yamamoto, J.
Direct Submission
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Homo sapiens cDNA FLJ38259 fis, clone FCBBF3001302, highly similar
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/db_xref = "taxon:9606"
/clone = "FCBBF300.302"
/tissue_type="brain"
/clone_lib="FCBBF3"
/dev_stage="fetal"
                                                                                                                                                                                                                                                                           /note="cloning vector:
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sphingosine kinase; SPK gene.
Homo sapiens.
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AJ245504
AJ245504.1 GI:801
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FSVLSLAWGFILAVDLESEKYRRLGEMRETLGFFLRLAALRTYRGRLAYLPVGRKVGSK
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FAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL"

a 422 c 462 g 297 t
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/db_xref="GI:8017376"
                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
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                                                                                       CCAAACTACTTCTGGATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAG
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                                                                                                                                                                                                                                          Vector: pMEIBS-FL3 (ACC.NO. AB009864)

R. Site1: DraIII (CACTGTCTG)

R. Site2: DraIII (CACTGTCTG)

R. Site2: DraIII (CACTGTCTG)

R. Site2: DraIII (CACTGTCTG)

R. Site3: DraIII (CACTGTCTG)

R. Site4: DraIII (CACTGTCTG)

R. Site5: DraIII (CACTGTCTG)

RESCRIPTION: Ist strand cDNA was primed with an oligo(dT) primer for greater for a synthesized with specific strand size selection was synthesized using specific 5'and 3' primers and amplified by PCR. The PCR product was digested with SiII and size selection was performed to exclude fragments (1.5kb. The SIII digested PCR product was cloned into distinct DraIII sites of pMEIBS-FL3. XhoI sites just outside the DraIII sites can be used to isolate the CDNA insert. Libraries were constructed by Sugano et al.(University of Tokyo, Institute, of Medical Science). Custom primer used for sequencing (5' end primer [CGACCTGCAGCTCGAGCACAA]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infectious Diseases, Division of Genetic Resources: 23-1, Toyama I-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mall:khashlenh.go.jp, ORL:http://www.nlh.go.jp/yoken/genebank/.Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-11181) URL: http://www.nlh.go.jp/yoken/genebank/.URL:
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MACAGA ESSCICULARIS
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Eukaryota: Metazoa: Primates; Catarrhini; Cercopithe
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CFUR insert sequence).
Macaca fascicularis adult cDNA to mRNA, clone_lib:macaque brain cDNA library OccE clone:OccE-16602.
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Isolation of full-length cDNA clones from macaque brain cDNA libraries
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Submitted (14-JUL-2000) Katsuyuki Hashimoto,
Infectious Diseases, Division of Genetic Res
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2 (bases 1
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Lab host:
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Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S
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mme: macaque brain cDNA library QccE
                                                                    /clone_lib="macaque brain cDNA library QccE"
/dev_stage="adult"
628. .1617
/codon_start=1
/product="unnamed protein product"
/protein_id="BAB01607.1"
                                                                                                                                       /clone="QccE-16602"
                                                                                                                                                             ∕organism="Maċaca fascicularis"
∕db_xref="taxon:9541"
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GGCTTCGGGGCTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCCTTCATTGCTGATGT
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/translation="MDPAGGPRGVLPRSCRVLVLLNPRGGKGKALQLFRSHVQPLLAE
AEISFTLMLTERRNHARELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQ
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KELCSLYAGGFIADVDLESEKYRRLGEMRETLGTELAALRTYRGRLAYLFVGRA
GSKTEVSPVVQQGPVDAHLVPLEEFVPSHWTVVPDQDFYLVLALLHSHIGSEMFAAP
MGRCAAGVMHLIFVPRAGVSRAMLLRLFLAMEKGRHMEYECPYLVFISGWGIDG"
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92.3%;
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Pred. No. 2e-2
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                                                                                                                  Mammalia; Butheria; Primates; Laurentes | 
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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AF200328.1 G
10947957
2 (bases 1 to 1173)
Pitson, S.M., D'Andrea, R.J.,
Gamble, J.R., Vadas, M.A. and
Direct Submission
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                         Vandeleur,L.,
Wattenberg,B.
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                                  GGCACCTTCCTGCGTCTGGCAGCCCTGCGGACCTACCGGGGCGGACTGGCCTACCCTTCCCTT 771
                                                                                                   GCTGATGTGGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTG
                                                                                                                                                                   CTGCACACGGCTTCGGGGCTGCGCCTCTTCTCTGTGCTCAGCCTGGCCCTGGGGGCTTCATT 651
                                                                                                                                                                                                                 GCGCTGGCAGCTTCCTTGAACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTC
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                                                                                GCTCATCTGGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGGAGATGCGCTTCACTCTG
                                                                                                                                                  CTGCACACGCCTTCGGGGCTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCCTTCATT
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/product="sphingosine kinase"
/product="sphingosine kinase"
/protein_id="aag01980.1"
/db_xref="GI-9909361"
/translation="MDPAGGPRGVLPRPCRVLVLLNPRGKGKALQLFRSHVQPLLAE
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LRLFESVLSLAWGFTADVDLESEKYRRLGEMRETLGTFLRLAALRTYRGRLAYLPVGRV
GSKTPASPVVVQQGPVDAHLVPLEEPVESHWTVVPDEDFVLVLALLHSHLGSEMFAAP
GSKTPASPVVVQQGPVDAHLVPLEEPVESHWTVPDEDFVLVLALLHSHLGSEMFAAP
GSKTPASPVVVQQGPVDAHLVPLEEPVESHWTVPDEDFVLVLYLHSHLGSEMFAAP
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349 c 390 g 246 t
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/db_xref="taxon:9606"
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Pred. No. 5e-207;
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Patent: WO 0131029-A 2 03-MAY-2001;
WARNER-LAMBERT COMPANY (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1155)
Allen,J., Gosink,M., Melendez,A.J. and Takacs,L.
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Series:
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Tissue Procurement: ATCC/DCTP/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephan
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Contact: MGC help des
Email: cgapbs-r@mail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission Submitted (01-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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1. (bases 1 to 1192)
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/protein_id="AAH04112.1"
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/translation="GTR9E663"
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EDFVLYLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLR-EFLAMEKGRHM
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/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
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/db_xref="taxon:9606"
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AC068145 IB3443 bp DNA linear HTG 04-MAY-20 HOMO Sapiens chromosome 17 clone CTD-2531H7 map 17, WORKING DRAFT SEQUENCE, 48 unordered pleces.
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                                                                     * NOTE: This is a 'working draft' sequence. It currently
* consists of 48 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1059: contig of 1059 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 5, 2000 this sequence version replaced gi:7960325.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Mammalla; Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 183443)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: Phrap; version 0.960731 Consensus quality: 152281 bases at least 040 Consensus quality: 167680 bases at least 030 Consensus quality: 174098 bases at least 030 Insert size: 200000; agarose-fp Insert size: 178743; sum-of-contigs Quality coverage: 2.9 in 020 bases; agarose-fp Occupant Coverage: 2.9 in 020 bases; agarose-fp Occupant
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                                                                                                                                                                                                                                                                                                        Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
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1 1059: contig of 1059 bp in length
1060 1159: gap of 100 bp
1160 2777: contig of 1618 bp in length
2778 2877: gap of 100 bp
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956 57055: gap of 100 bp
16 62913: contig of 358 bp in length
4 62813: gap of 100 bp
1 66519: contig of 3706 bp in length
66619: gap of 100 bp
66619: contig of 3706 bp in length
66619: contig of 3706 bp in length
66619: gap of 100 bp
66619: contig of 3706 bp in length
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40521: contig of 2447 bp in length
22 40521: gap of 100 bp
22 43219: contig of 2598 bp in length
20 43319: gap of 100 bp
20 43319: gap of 200 bp in length
20 46161: contig of 2842 bp in length
20 46261: gap of 100 bp
21 48463: contig of 202 bp in length
22 48463: contig of 2712 bp in length
23 48463: gap of 100 bp
24 48563: gap of 2712 bp in length
25 4853: gap of 2712 bp in length
                                                                                                                                                                                                                                                     20 68930: contig of 2
31 69030: gap of 10
31 72724: contig of 3
25 72824: gap of 10
25 7692: contig of 3
3 76192: gap of 10
3 80143: contig of 3
     y3428: contig of 4

19 93528: gap of 10,

9 97177: contig of 3(

8 97277: gap of 10,

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8215: con
8315: gap of
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5447:
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27431: gap of 100 bp
30406: contig of 2975 bp in length
30506: gap of 100 bp
32805: contig of 2299 bp in length
32905: gap of 100 bp
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53622: gap of 100 bp in 1.
53662: gap of 100 bp 1
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1894: gap of
16857: cr
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3507: gap of 100 bp in le
25455: contry of 1948 bp in le
35555: gap of 100 bp
35555: gap of 1776 bp in le
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21460: contig of 1170 i
1560: gap of 100 bp
22407: contig of 1847 i
3507: gap of 100 bp
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24: gap of
93428:
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957: gap of 100 bp
18266: contig of 1309 1
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243: gap of
84957: contig of
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f 1847 bp in length
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743 CCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTCCAAGACACCTGCCT 802
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159466 159565; gap of 13120 bp
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/db_xref="taxon:9606"
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13895. .16857
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159465: contig of 10631 k
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148734: conti
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132364: contig of 7739 bp
132464: gap of 100 bp
132464: gap of 7024 bp
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OY 1223 GCGTGGACCCCCCCCCCCACTGAAGCCCCAGCAATGCCACCACAACAACACCCCTTAT 1282
Db 133497 GCGTGGAGCCCCCGCCCAGCTGGAAGCCCCCAGCAACAAGAGCCCTTAT 133438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OY 1163 TGGTTAGCGAGGCCGTGCAGGCCAAGGTCCACCCAAACTACTTCTGGATGGTCCAGCGGTT 1222
Db 133557 TGGTTAGCGAGGCCGTGCAGGGCCAGGTCCACCCAAACTACTTCTGGATGGTCAGTCGTT 133498
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Db 133797 ACTCGCACCTGGGCAGTGAGATGTTTGCTGCACCCAGTGGGCCGCTGTGCAGCTGACCTCA 133738
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Oy 1523 CGAACCAAATCCAAATAAAGTCACATTCCCACCCTG 1558
Db 133197 CGAACCAAATCCAAATAAAGTGACATTCCCAGCCTG 133162
                                                                                                                                              Db 133257 GCTGGCTGGCCCAGCTGCCTATGTAAGGCCTTCTAGTTTGTTCTGAGACCCCCACCCCA 133198
                                                                                                                                                                                                                                                                                             Db 133317 GAAGGTGGAGGCTATGCTTTGGGGGGACAGGCCAGAATGAAGTCCTGGGTCAGGAGCCCA 133258
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Search completed: May 17, 2003, 13:39:06 Job time: 4577 secs

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Result
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Perfect score:
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RESULT 2 PCT-US95-04801-3

Sequence 3, Application PC/TUS9504801
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Martin, Juan F.
APPLICANT: Coque, Juan R.
APPLICANT: Enguita, Francisco J.

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Sequence 1, Application US/08209747 Patent No. 5733771
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                                                                                                             GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
TITLE OF INVENTION: CDNAS Encoding Minor Ampullate Spider
TITLE OF INVENTION: SILK Proteins
NUMBER OF SEQUENCES: 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 900 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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NAME: Wallen III, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19179
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT' APPLICATION DATA:
                                                                                                     CORRESPONDENCE ADDRESS
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 GCGGCCGACGACCCGGCCGCCCAGTCCCCGCACCAGCGGGTGCACGTGGACCAGAGCCCG 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 CGCGGCGGCAAGGCCTTGCCAGCTCTTCCGGAGTCACGTGCAGCCCCTTTTTGGCT 258
                                     STREET; P.O. Box 7. CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: John W. Wallen III
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US95/04801 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                           EE: Birch, St.
P.O. Box 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Puente, Juan L.
Llarena, Francisco J.
Liras, Paloma
IVENTION: DNA ENCODING CEPHAMYCIN BIOSYNTHESIS
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                                                                               Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Release #1.0, Version #1.25
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RESULT 4
US-08-458-298-1
US-08-458-298-1
Sequence 1 Application US/08458298
Patent No. 5756677
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
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Best Local Similarity
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC COMPSTONS DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,747
FILING DAYE: 14-MAR-1994
CLASSIFICATION: 530
ATTORNEY/ACENT INFORMATION:
NAME: MUTPBY Jr., Gerald M.
REGISTRATION NUMBER: 28.977
REFERENCE/DOCKET NUMBER: 1447-104P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 145;
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INFORMATION FOR SEQ ID NO: 1:
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NAME/KEY: CDS
LOCATION: 183..2675
OTHER INFORMATION: /product= "N. clavipes minor
OTHER INFORMATION: ampullate silk protein"
                                                                                                                                                                                                                            1631 GCAGGTGC 1638
                                                                                                                                                                                                                                                                                                                 1571 GCCGGAGGCGCTGGTTACGGTAGAGGTGCTGGTGCTGGAGCTGGTGCCGCTGCTGGG 1630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1391 GGTGCAGGAGCTGGTGCGGCTGCTGCTGGAGCAGCAGCTGGAGGCGCTGGTGGTTAC 1450
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                  1511 GGTCAAGGTGGATACGGTGCCGGAGCAGGAGCTGGTGCTGCTGCAGCTGCTGCAACAGGA 1570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
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                                                                                                                                                                                                                                                                                                                                         345 GGACGCTCTGGTGGTCATGTCTGGAGACGGGCTGATGCACGAGGTGGTGAACGGGCTCAT 404
                                                                                                                                                                                                                                                                                                                                                                                                                              405 GGAGCGGC 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE: minor ampullate gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 163; Indels
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PCT-US95-04801-3

RESULT 3 US-08-209-747-1

ADDRESSEE:

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US-08-458-298-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 703-205-8000
TELEPAX: 703-205-8050
(INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2793 base pairs
                                                                                                                                                                                                                     1391
                                                                                          1511
                                                                                                                                                       1451
                                                                                                                                                                                                                                                                               1331 GCAGGAGCCGCTGCGGGTGCAGGAGCCTGGAGGCTACGGTGGTCAAGGTGGGTACGGTGCC 1390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CU
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 56
CORRESPONDENCES: 56
                             1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                     165
405
                                                                                                                                                                                      225
                                                                                                                                                                                                                                                                                                             LOCATION: 183..2675
OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Nephila clavipes
TISSUE TYPE: minor ampullate gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977 REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 02-JU
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                                                                                                                                                                                                                                    GCGGCCCTGCCGCGTGCTGGTGCTGCAACCCGCGGCGGCGAAGGGCAAGGCCCTTGCA 224
                                            GGACGCTCTGGTGATGTCTGGAGACGGGCTGATGCACGAGGTGGTGAACGGGCTCAT 404
                                                                                                         GCTCACTGAGCGGCAGCACGCGCGGGGAGCTGGGGCCGCTGGGCCGCTGGGCCGCTGGGCCGCTGGGCCGGAGGAGCTGGGAGGAGCTGGGCCGCTGGGCCGCTGGGCCGCTGGGCCGCTGGGCCGCTGGGCCGCTGGGCCGCTGGGCCGCTGGGCCGCTGGGAGGAGCTGGGCCGCTGGGCCGCTGGGAGGAGCTGGGCCGCTGGGAGGAGCTGGGCCGCTG
                                                                                                                                                    GGTAGAGGTGCTGGTGCTGGAGCTGGAGCTGCAGGCGCAGGAGCTGGAGGCTACGGT 1510
                                                                                                                                                                                                                  GGTGCAGGAGCTGGTGCGGCTGCTGCTGCAGGAGCAGGAGCTGGAGGCGCTGGTTAC 1450
                          GCCGGAGGCGCTGGTTGCGTAGAGGTGCTGGTGCTGGAGCTGGTGCCGCTGCTGGG
                                                                                        GGTCAAGGTGGATACGGTGCCGGAGCAGGAGCTGGTGCTGCTGCAGCTGCAACAGGA
                                                                                                                                                                                   GCTCTTCCGGAGTCACGTGCAGCCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGAT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: Birch, Stewart, Kolasch & Birch
r: P.O. Box 747
Falls Church
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                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                              Score 47.2;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         silk protein"
                                                                                                                                                                                                                                                                                                                                                                .044;
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5215881-2/c
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US-07-945-283-1/c
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                                                                                                                                                                                                                Sequence 1, Application US/07945283 Patent No. 5352596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Cheung,
APPLICANT: Wesley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PSEUDORABIES DIAGNOSIS PROBES NUMBER OF SEQUENCES: 3
STREET: LUL-
STREET: Peoria
CITY: Peoria
                                                                                                                         TITLE OF INVENTION:
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                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1268 CGTGGAGACCCACCGGC
                                                                                                    NUMBER OF SEQUENCES:
                             ADDRESSEE: Curranter 1815 No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 13-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                     ATTGCTGTGCCGCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCCGGGGCCGAGCCGCTGCGCCTCTGCCGCCAGGACAACGTGCGCTACACGGTGAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                            GGCCGTGCGCTGGGACTTTGCGCCCCTTCGAGACCAGCGTCCGCCGCCGCCGGCGGCGGCGC 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                           ANDREW K
                                                                                                                                                         Andrew K. Ronald D.
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                                                                                                                     Involving
                                                                                                                                         Pseudorabies Virus Deletion Mutants
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Pred. No.
                                                                                                                       The
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                                                                                                                       EP0 and LLT Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.14;
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COUNTRY:

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US-07-945-283-1
                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 2.9%; Score 45; DB 1; Length 8438; Best Local Similarity 44.5%; Pred. No. 0.19; Matches 221; Conservative 0; Mismatches 275; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEO ID NO: 1: SEQUENCE CHARACTERISTICS: SEQUENCE: .8438 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-885-4011 ext.513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07
APPLICATION NUMBER: US/07
FILING DATE: 19920911
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                   2971 CCCCACCGTGGACGGCTGCAAGGACATGGCCCGCCAGCGCTCCGCGCTCGGGGCTCGGGGA 2912
                                                                                                                                                                                                                                                         3091 CCCCGGGGCCGAGCCGCTGCGCCTCTGCCGCCAGGACAACGTGCGCTACACGGTGAGCAC 3032
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FEATURE:
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MEDIUM TYPE: Floppy
                                      2851 CGCCCCGCTGCGGCCCGTCTTCGTCTCCTGCGGGCCCGGGGGCCTCGCCGAGCTCCGCGG 2792
                                                                                                             2911 CCCGGACTTTGACGCGGGCGCCCCCTTCGGGCCACCGCGGCCCAACCGCTGGGGGCCTCGG 2852
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                                                                                                                                                                                                      189 GCTGAACCCGCCGCCGCCAAGGCCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCC 248
                                                                                                                                                                                                                                                                                             130 ATGGATCCAGCGGGCGGCCCCCGGGGGCG-TGCTCCCGCGGCCCTGCCGCGTGCTGGTGCT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTI - SENSE:
                                                                                                                                               249 CCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGC 308
  369 AGACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGGCCTGACTGGGAGACCGC 428
                                                                          309 GCGGGAGCTGGTGCGGTCGGAGGAGCTGGGCCCCTTGGACGCTCTGGTGGTCATGTCTGG 368
                                                                                                                                                                                                                                                                                                                                                                 70 CACGGGCAGCGCCCACAGCGCCAGGGACCCCCTGGCAGCGGGAGCCGCGGGTCGAGGTT 129
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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replace(1381,
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                                                                                                                                                                                                                                                               TELEPAX: (415) 327-2951
TELEX: 706141
INFORMATION FOR SEQ JD NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/07640476 Patent No. 5376536
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                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kate H. Murashige
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2469
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEPAX: (415) 327-2951
                                                                                                                                                                                                                     STRANDEDNALL INCAR TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2671 GGCCGTGCGCACTTTGCGCCCTTCGAGACCAGCGTCCGCGCCGCCGCCGGCGGCGC
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0,
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: QUAX, WILHELMUS APPLICANT: LUITEN, RUDOLF
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SCHUURHUIZEN, PAUL W. APPLLICANT: MRABET, NOADIR TITLE OF INVENTION: OF INVENTION: THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
  LOCATION: 1.1164
IDENTIFICATION METHOD:
OTHER INFORMATION: /EC.
OTHER INFORMATION: /PXC
OTHER INFORMATION: /PXC
OTHER INFORMATION: /Sta
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                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER FILING DATE: 19910
                                                                                                                                              ORGANISM: Streptomyces murinus
STRAIN: DSM 40091
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ZIP: 94025
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                                                                                              NAME/KEY: CDS
LOCATION: 1...
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545 Middlefield Road, Suite 200
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/EC_number= 5.3.1.5
/product= "xylose isomerase (glucose isomerase)"
/evidence Experisional
/standard_name= "D-xylose ketol isomerase"
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                                                                             experimental
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                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 08/3///
APPLICATION NUMBER: US 08/3///
FILING DATE: 24-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
NAME: GOLDBERG, JULES E.
24,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MIKOLAJC:
APPLICANT: ARMENTROU
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                           TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 1:
                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 28804 base pai
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ADDRESSEE: JULES E.
                 TOPOLOGY: u
                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 212-986-4090
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                                                                    LENGTH: 28804 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 261 MAI
CITY: NEW YORK
                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTGAACGGGCTCATGGAGCGGCCTGACTGGGAGACCGCCATCCAGAAGCCCCCTGTG 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGCTGGGCCGCTGGGACGCTCTGGTGGTCATGTCTGGAGACGGGCTGATGCACGAGGT 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10016-2391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: JULES E GOLDBERG
261 MADISON AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIKOLAJCZAK, MARCIA
ARMENTROUT, RICHARD W.
IVENTION: DNA SEGMENTS AND METHODS FOR INCREASING
IVENTION: POLYSACCHARIDE PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAMAZAKI, MOTOHIDE THORNE, LINDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLLOCK, THOMAS J.
                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
N-terminal
                 DNA (genomic)
                                                      unknown
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46.8%;
                                                                                                                                                                                                                                                                                  US 08/377,440
                                                                                                                                                                                                                                                                                                                                                           US/08/592,874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44.2;
Pred. No. 0.
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US-09-096-867-2
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; ORGANISM: Sphingomonas
US-09-096-942-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09096942
Patent No. 6027925
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.7%;
Best Local Similarity 49.5%;
Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas Bacteria TITLE OF INVENTION: Carrying Genes from Xanthomonas Campestris FILE REFERENCE: seeq list for appl filed from pro. appl CURRENT APPLICATION NUMBER: US/09/096,942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yamazaki, Motohide APPLICANT: Thorne, Linda
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APPLICANT: Mikolajczak, Marcia
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                                                                                                                                                                     LENGTH: 28804
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                                                                                                                           344 GGGACGCTCTGGTGGTCATGTCTGGAGACGGGCTGATGCACG
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                                                                                      GGGGCGCAGTGATCGTCGGCTTCCTCGGCGTGCTGATCGTCG
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Sequence 2, Application US/09096867 Patent No. 6030817

GENERAL INFORMATION:

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US-08-804-227C-1
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; ORGANISM: Sphingomonas sp. S88
US-09-096-867-2
                                          CUMPUTER: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/804,227.
FILING DATE: February 21, 1000
CLASSIFICATION: 435
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08804227C Patent No. 5876991 GENERAL INFORMATION:
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LENGTH: 28804
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Best Local 9
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APPLICANT: Mikolajczak, Marcia
APPLICANT: Mikolajczak, Marcia
APPLICANT: Mikolajczak, Marcia
APPLICANT: Thorne, Linda
APPLICANT: Thorne, Linda
APPLICANT: Armentrout, Richard W
TITLE OF INVENTION: Production of Xanthan Gum by Sphingomonas Bacteria
TITLE OF INVENTION: Carrying Genes from Xanthomonas Campestris
FILE REFERENCE: Seq list for appl filed from pro. appl
CURRENT APPLICATION NUMBER: US/09/096,867
CURRENT APPLICATION NUMBER: US/09/096,867
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EARLIER FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: x-8231
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
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STREET: LILLY CORPORTY: INDIANAPOLIS
STATE: IN
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                                                                                                                                                                                                                                                                                                            USA .
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                                                                        : US/08/804,227C
: February 21, 1997
ON: 435
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US-08-949-155-49/c
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Patent No. 6271436
GENERAL INFORMATION:
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Best Local
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TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 1:
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FEATURE:
NAME/KEY:
                 COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC COMPALIBLE
COMPUTER: LBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                         TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Generation of Transgenic Animal Species NUMBER OF SEQUENCES: 51
                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE AND DURKEE STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                  APPLICANT: Piedrahita, Jora APPLICANT: Bazer, Fuller W
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                                                                                                                                    STREET: P.O. I
CITY: Houston
STATE: TX
    SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36249..41774
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31232.,36067
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816..14234
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48.0%;
                                                                                                                                                                                                                                                                                                        Jorge A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 132; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42.8; DB Pred. No. 0.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 43280;
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CURRENT APPLICATION DATA:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 49, Applicati
Patent No. 6369294
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1482 GGCGGCCGCCACCCGGC 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1542 GGGGCCCGGGCGGGCTGGGCGCAGGTGCGGGACCATGTGCCCGCGCTCGCCCCCGGC 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 4791 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000 TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/046,094 FILING DATE: 09-MAY-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,338
FILING DATE: 11-OCT-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 GGCGTGCTCCCGCGGCC 170:
                                                                     COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/819,964
FILING DATE: 28-Mar-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION: APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: SIU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 CAGCACCGATAAGGAGCTGAAGGGCAGGGGAGCGCCACGGGCAGCGCCCACAGCGCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 2.7%;
Local Similarity 56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/949,155 FILING DATE: Concurrently Herewit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Piedrahita, Jorge A
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                        CITY: Houston
APPLICATION NUMBER: US 60/046,094 FILING DATE: 09-MAY-1997
                                   APPLICATION NUMBER: 08/949,155 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                      COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: ARNOLD, WHITE AND DURKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09819964
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Compositions and Methods for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42.6; DB 4; Pred. No. 0.6;
                                                                                                                                                                     Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                        Animal Species
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                                                                                                                                                                                                        US-09-420-211-1
                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
                                                                                                                                     Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09420211B Patent No. 6303330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Croteau, Rodney
APPLICANT: Burke, Charles C
APPLICANT: Wildung, Mark R
                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/420,211B
CURRENT FILING DATE: 1999-10-18
EARLIER APPLICATION NUMBER: PC/US98/21772
EARLIER FILING DATE: 1998-10-15
                                                                                                                                                                                                                                                                                                                                                              EARLIER FILING DATE: 1997-10-16 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GERANYL DIPHOSPHATE SYNTHASE LARGE SUBUNIT, AND METHODS TITLE OF INVENTION: OF USE FILE REFERENCE: WSUR14294
                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 08/951,924
                                                                                                                                                                                                                                                                     LENGTH: 1131
TYPE: DNA
ORGANISM: Mentha piperita
                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (713) 789-2
INFORMATION FOR SEQ ID NO: 49:
                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                        LOCATION: (1)..(1131)
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                            254 TGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCGGAACCACGCGCGGG 313
                                                                  521
                                                                                                   194 ACCCGCGCGGCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTCACGTGCAGCCCCTTT 253
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nes 78; Conserv
                                                                                                                                                       Local Similarity
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TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Hibler, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGCCCCGGGCGGGCTGGGCGCGAGGTGCGGGGACCATGTGCCCGCGCTCGCCCCCGGC 1483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4791 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 41,071 REFERENCE/DOCKET NUMBER: TA
                                                                                                                                     Conservative
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                                                                                                                                                    2.7%;
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                                                                                                                                     0;
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Pred. No. 0.
                                                                                                                                                       Pred. No.
                                                                                                                                                                    Score 42;
                                                                                                                                     Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                       0.55;
                                                                                                                                                                    DB 4; Length 1131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59;
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                                                                                                                                     Indels
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Qy Db Qy

641 CGCCGGAGCGGATCGTGAGGGTCCTCGGCGAGCTGGCTGTCTCGATCGGGTCGGAGGGGC 700

GGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGG 411

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US-07-918-023-1
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PStentin Release #1.0, Version #1.25

CURRENT AFPLICATION DATE:

APPLICATION NUMBER: US/07/918,023

FILING DATE: 19920724

CLASSIFICATION STAN:

APPLICATION NUMBER: CH 2247/91

FILING DATE: 26-JUL-1991

ATTONNEY/AGENT INFORMATION:

REGISTRATION NUMBER: LP 1521

TELECOMMUNICATION NUMBER: LP 1521

TELECOMMUNICATION NUMBER: LP 1521

TELECOMMUNICATION NUMBER: SJ.083

REFERENCE/DOCKET NUMBER: LP 1521

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 659-2015

TELEEX: 249748

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1843 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: $11016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/07918023 Patent No. 5427934 GENERAL INFORMATION:
NAME/KEY: mis_feature
LOCATION: 289..1566
PUBLICATION INFORMATION:
LOCUMENT NUMBER: IE 9224406
FILING DATE: 23.-UU-1992
RELEVANT RESIDUES IN SEQ ID NO: 1
PUBLICATION INFORMATION:
LOCUMENT NUMBER: JP 198717/92
FILING DATE: 34.-UUL-1992
RELEVANT RESIDUES IN SEQ ID NO: 1
PUBLICATION INFORMATION:
LOCUMENT NUMBER: PL P 295408
FILING DATE: 24.-UUL-1992
                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: D
ORIGINAL SOURCE:
ORGANISM: Comau
STRAIN: A:18
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zimmermann, Thomas
APPLICANT: Robins, Karen
APPLICANT: Birch, Olwen
APPLICANT: Birch, Olwen
APPLICANT: Boblen, Elisabeth
TITLE OF INVENTION: CENETIC ENGINEERING PROCESS FOR THE
TITLE OF INVENTION: PRODUCTION OF S-(+)-2,2-DIMETHYLCYCLOPROPANECARBOXAMIDE
TITLE OF INVENTION: BY MICROORGANISMS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Fisher, Christen & Sabol STREET: 2000 M Street, N.W., Suite 590 CITY: Washington STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
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PUBLICATION INFORMATION:
DOCUMENT NUMBER: RO 92-01033

FILING DAYE: 24-JUL-1992

RELEVANT RESIDUES IN SEO ID NO: 1: FROM 1 TO 1843

PUBLICATION INFORMATION:
DOCUMENT NUMBER: SU UNKNOWN

FILING DAYE: 24-JUL-1992

RELEVANT RESIDUES IN SEO ID NO: 1: FROM 1 TO 1843

PUBLICATION INFORMATION:
DOCUMENT NUMBER: CS PV2323-92

FILING DAYE: 24-JUL-1992

RELEVANT RESIDUES IN SEO ID NO: 1: FROM 1 TO 1843

PUBLICATION INFORMATION:
DOCUMENT NUMBER: CS PV2323-92

FILING DAYE: 24-JUL-1992

RELEVANT RESIDUES IN SEO ID NO: 1: FROM 1 TO 1843

PUBLICATION INFORMATION:
DOCUMENT NUMBER: HU P9202439

FILING DAYE: 24-JUL-1992

RELEVANT RESIDUES IN SEO ID NO: 1: FROM 1 TO 1843

PUBLICATION INFORMATION:
DOCUMENT NUMBER: HU P9202439

FILING DAYE: 24-JUL-1992

RELEVANT RESIDUES IN SEO ID NO: 1: FROM 1 TO 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.7%; Score 42; DB 1; Length 1843; Best Local Similarity 45.5%; Pred. No. 0.63; Matches 190; Conservative 0; Mismatches 225; Indels
                                                                                                                                                                                                                                                                      1366 GGACTTCACGGGCCGGGTGCGTGCACTCTTCGCGCAGGTGGATCTGCTGGTGCCCC 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1006 GCCCAGCCAGTGCAGCGTGCCCGACTATCTGGCCATGATGACGCGCGGATTCTCCGGCCT 1065
                                                                        1050 GAAGGGCAGGCATATGGAGTATGAATGCCCCCTACTTGGTATATGTGCCCGGTGGTCGCC 1107
                                                                                                                                       1306 GATOGACOTGGGGCTGGGCCTGTCCGCCACCGACTACCAGCGGCTGCTGCTGCGCCGCGC 1365
                                                                                                                                                                                                                                                                                                                                                                                                                      1186 TCCCGATGCCACCCAGGCGGTGGAGGACTGGCCGGCGCTGTGCGCGGTGGAGACCGCCGT 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 813 GCTCCAGCAGGGCCCGGTAGATGCACA----CCTTGTGCCACTGGAGGAGCCAGTGCCCTC 869
                                                                                                                                                                                                       990 GTTCTACGTGCGGGGGGGGTGTCTCGTGCCATGCTGCTGCGCCCTCTTCCTGGCCATGGA 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 753 CCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTCCAAGACACCTGCCTCCCCCCGTTGT 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCACTGGACAGTGGTGCCCGACGAGGACTTTGTGCTAGTCCTGGCACTGCTGCACTCGCA 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGGAGCAGGCCCTGGCGGTGGCGCAGCGCCTGGGGGGCCAGCGTGCAGGAGGTCCGCTT 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
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Search completed: May 17, 2003, 14:39:35 Job time: 391 secs

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Database
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0 seq length: 2000000000
       Published_Applications_Na:*

1: /cgn2_6/ptodata/1/pubpna/U

2: /cgn2_6/ptodata/1/pubpna/U

3: /cgn2_6/ptodata/1/pubpna/U

4: /cgn2_6/ptodata/1/pubpna/U

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1573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Listing first 45 summaries
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/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

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43.8	43.8	43.8	43.8	43.8	44.8	193	193	197.4	197.4	246.8	262.8	262.8	291	387.6	768	853.2	1155	1511.6	Score
2.8	2.8	2.8	2.8	2.8	2.8	12.3	12.3	12.5	12.5	15.7	16.7	16.7	18.5	24.6	48.8	54.2	73.4	96.1	Query Match
6823	4372	3132	2916	2898	88421	296	296	199	199	2698	2380	1857	480	394	1149	1759	1155	1600	Query Match Length
9	10	10	10	10	9	10	9	9	9	10	10	10	10	10	10	10	10	10	DB
us-09-989-920-16 .	US-09-993-811-1	US-09-737-149-7	US-09-737-149-5	US-09-737-149-3	US-09-976-059-1	US-09-777-564-658	US-10-015-219-658	US-10-040-862-2905	US-09-796-692-2905	US-09-817-676A-11	US-09-817-676A-13	US-09-970-516-3	US-09-783-590-9248	US-09-954-456-1756	US-09-970-516-5	US-09-784-810A-3	US-09-970-516-1	US-09-784-810A-1	ID
Sequence 16, Appl	Sequence 1, Appli	Sequence 7, Appli	Sequence 5, Appli	Sequence 3, Appli	Sequence 1, Appli		Sequence 658, App	Sequence 2905, Ap	٠.	11	Sequence 13, Appl	Sequence 3, Appli	Sequence 9248, Ap	Sequence 1756, Ap	Sequence 5, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Description

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2436	2436	2436	2436	2436	2436	2436	2436	2436	2436	2436	2436	2436	2436	2436	629	1990	1903	1874	520	520	4403	1131	471	2862	1
9 US-10-173-700-309	9 US-10-180-557-309	9 US-10-180-552-309	9 US-10-176-913-309	US-10-	9 US-10-176-482-309	US-10-	-Su	9 US-10-173-706-309	9 US-10-063-502-99	9 US-10-175-737-309	9 US-10-063-616-99	9 US-10-176-758-309	9 US-10-174-590-309	9 US-10-063-547-99	US-(10 US-09-822-830A-621		9 US-10-184-634-332	9 US-10-184-644-332	10 US-09-880-107-2402	10 US-09-934-778-1	9 US-09-918-995-11975	10 US-09-888-615-7	
Sequence 309, App	Sequence 309, App	Sequence 309, App	Sequence 309, App	Sequence 309, App	`	-		309,		Sequence 309, App	Sequence 99, Appl	-		Sequence 99, Appl	ъ	Sequence 39, Appl	Sequence 621, App	Sequence 33, Appl	Sequence 332, App	Sequence 332, App	Sequence 2402, Ap	Sequence 1, Appli	Sequence 11975, A	Sequence 7, Appli	added to a contract

ALIGNMENTS

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SEQ ID NO 1
LENGTH: 1600
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-784-810A-1
                                                                                                                                                                                                                                                   US-09-784-810A-1
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APPLICANT: RASTELLI, LUCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09784810A
Patent No. US20020082203A1
                                                                                                                                                                                     Best Local Similarity
Matches 1534; Conserv
                                                                                                                                                                                                    Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING TITLE OF INVENTION: SAME FILE REFERENCE: 10716-08
CURRENT APPLICATION NUMBER: US/09/784,810A
CURRENT FILING DATE: 2001-02-14
CURRENT FILING DATE: 2001-02-14
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/191,261
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/182,360 PRIOR FILING DATE: 2000-02-14
                                                                                                                                                                                                                                                             NAME/KEY: modified_base LOCATION: (1)
OTHER INFORMATION: a, t,
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 166
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                                                                                          AGCCGCCGCCACGGGCAGCG-CCCCACAGCGCCAGGGACCCCCTGGCAGCGGGAGCCGCG
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98.78;
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Pred. No. 0;
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                                                                                             GTTTGCAGTGGATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCCAGGTGCACCCAAA 1199
                                                                                                                                                   CTACTTGGTATATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCCAAGGATGGGAAAGGTGT 1185
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                                                                         GTTTGCAGTGGATGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCCAGGTGCACCCAAA 1245
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Patent NO. US20020099029A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NO. US2002009029A1artis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration of TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REPERENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOCTWARE: PatentIn version 3.1
SEQ ID NO 1155
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 1155;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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                                               ATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGCCTCTGGCAACGCGCTGGCAGCTTCCTTG
                                                                                                               GACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAACGGGCCTGACTGGGAGACCGCC 429
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AACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTA 549
                              ATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCCTTG
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Sequence 3, Application US/09784810A
Patent No. US20020082203A1
GENERAL INFORMATION:
APPLICANT: RASTELLI, LUCA
TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES
TITLE OF INVENTION: SAME
FILE REFERENCE: 10716-08
CURRENT APPLICATION NUMBER: US/09/784,810A
CURRENT APPLICATION NUMBER: US/09/784,810A
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/182,360
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEG ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
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; SEQ ID NO 3; LENGTH: 1759; TYPE: DNA; ORGANISM: MUS n US-09-784-810A-3
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Best Local Similarity 73.
Matches 1158; Conservative
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Pred. No. 6.3e
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US-09-970-516-5

Sequence 5. Application US/09970516

Patent No. US20020099029A1

GENERAL INFORMATION:
APPLICANT: No. US20020099029Alartis AG
APPLICANT: No. US20020099029Alartis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
FILE REFERENCE: 4-31617

CURRENT APPLICATION NUMBER: US/09/970,516

CURRENT FILING DATE: 2001-10-04

NUMBER OF SED ID NOS: 6

NUMBER OF SED ID NOS: 6

SECTION FRANCE: Patentin version 3.1
                                                                                                     ; NAME/KEY: CDS
; LOCATION: (1)..(1149)
; OTHER INFORMATION:
US-09-970-516-5
                                                                                                                                                                             SEQ ID NO 5
LENGTH: 1149
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
                         Query Match
Best Local Similarity
Matches 919; Conserv
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ilarity 79.8%;
Conservative
                  Score 768; DB 10;
Pred. No. 3.9e-205;
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1210 ATGGTCAGCGGTTGCGTGGAGCCCCCGCCCAGCTGGAAGCCCCAGCAGATGCCACCGCCA 1269
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Best Local
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LENGTH: 394
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                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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NUMBER OF SEQ ID NOS: 2276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canoritle OF INVENTION: Sets
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APPLICATION NUMBER: US/60/235,134
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TGGCTGGGCCCAGCTGCCTATGTAAGGCCTTCTAGTTTGTTCTGAGACCCCCACCCCACG
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PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9248
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APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REPERENCE: PO-16 2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
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                   LOCATION: (356)
COTHER INFORMATION: n equals
NAME/KEY: misc feature
TOCATION: (367)
                                                                                                                                                                                  LOCATION: (337)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals
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             LOCATION: (367)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                         LOCATION: (350)
OTHER INFORMATION: n equals
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misc feature
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                                                                      a,t,g,
                                                                                                                             a,t,g,
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RESULT 7
US-09-970-516-3
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                 Sequence 3, Application US/09970516
Patent NO. US2002099029A1
GENERAL INFORMATION:
APPLICANT: NO. US20020099029Alartis AG
APPLICANT: NO. US20020099029Alartis AG
TITLE OF INVENTION: Induction of blood vessel formation through administration
TITLE OF INVENTION: polynucleotides encoding sphingosine kinases
TILE REFERENCE: 4-31617
CURRENT APPLICATION NUMBER: US/09/970,516
CURRENT FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
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Best Local s
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LOCATION: (400)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (412)
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LOCATION: (391)
OTHER INFORMATION: n equals a,t,q, or
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LOCATION: (386)
OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (384)
OTHER INFORMATION: n equals a,t,g, or c
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  LENGTH: 1857
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430 GTANTCGGGTTTTGGGGAAATNGGTTTAATTTTGGGAAATTTC 472
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Local Similarity 86.4%; Pred. No. 9.2e-72;
Nes 400; Conservative 0; Mismatches 55;
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LOCATION: (1)..(18
OTHER INFORMATION:
US-09-970-516-3
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                                                                                                                           Sequence 13, Application US/09817676A
Patent No. US20020042101A1
GENERAL INFORMATION:
APPLICANT: Spiegel, Sarah
APPLICANT: Kobama, Takafumi
APPLICANT: Kobama, Takafumi
TITLE OF INVENTION: Mammallan Sphingosine Kinase Type 2 Isoforms, Cloning,
TITLE OF INVENTION: Expression and Methods of Use Thereof
FILE REFERENCE: 00170/HG
                 CURRENT APPLICATION NUMBER: US/09/817,676A CURRENT FILING DATE: 2001-03-26 PRIOR APPLICATION NUMBER: US.60/194,318 PRIOR FILING DATE: 2000-04-03 NUMBER OF SEQ ID NOS: 15
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Best Local
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Homo sapiens
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es 399; Conserv
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63.7%;
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RESULT 9
US-09-817-676A-11
: Sequence 11, Application US/09817676A
; Patent No. US20020042101A1
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Best Local Sin
Matches 399;
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DATABASE ENTRY DATE: 2000-06-27
-09-817-676A-13
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NAME/KEY: CDS
LOCATION: (7)..(1860)
PUBLICATION INFORMATION:
TITLE: Molecular cloning and functional characterization
TITLE: novel mammalian sphingosine kinase type 2 isoform
JOURNAL: J. Biol. Chem.
VOLUME: 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2380
TYPE: DNA
ORGANISM: Homo sapiens
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PAGES: 19513-19520
DATE: 2000-06-30
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TH: 2380
                                                                                                                                                                                                                                                                                                                                                                                                                          CATCCTCCCTGCGGCTCGGGCAACGCGCGTGGCCGGAGCAGTGAACCAGCAGCAGCAGGGGGGATT
INFORMATION:
                                                                                                          CCGCGGACGCCTCTCCTACCTCCCCG 1039
                                                                                                                        CCGCGGCCGACTGGCCTACCTCCCTG
                                                                                                                                                                      CTTGGGCAGTGCCCGCTTCACACTGGGCCACGCTGCGGCCTCGCCACACTGCACACCTA
                                                                                                                                                                                        TCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTTCGGCAGCCTGCGCACCTA 746
                                                                                                                                                                                                                                                 GCTCAGCCTGGGCCTTCATTGCTGATGTGGACCTAGAGAGTGAGAGTATCGGCG
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63.7%;
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Pred. No. 9.9e-64;
0; Mismatches 227;
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; ISSUE: 26
; PACES: 19513-19520
; DATE: 2000-06-30
; DATABASE ACCESSION NUMBER: AF245448
; DATABASE ENTRY DATE: 2000-06-27
US-09-817-676A-11
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В
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Best Local Similarity 62.1%;
Matches 389; Conservative
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LENGTH: 2698
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PRIOR FILLING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/817,676A CURRENT FILING DATE: 2001-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
TITLE: Molecular cloning and functional characterization of
TITLE: novel mammalian sphingosine kinase type 2 isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Mammalian Sphingosine Kinase TITLE OF INVENTION: Expression and Methods of Us FILE REFERENCE: 00170/\mathrm{HG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Spiegel, APPLICANT: Kohama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL: J. Biol. Chem VOLUME: 275
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LOCATION: (387)..(2237)
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                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGGTGAACGGGCTCATGGAGCGGCCTGACTGGGAGACCGCCATCCAGAAGCCCCCTGTG 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGGGGCCTGGCCTGGCAGCGCTGTATGGACCACGTGGTGCCAATGATCTCTGAAGCTGG 916
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CCTGGGCAGCGCTCGATTCACACTGGGTGCAGTGCTAGGCCTGGCCTCGTTGCATACCTA
                     TCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTGGGAGCCCTGCGCACCTA 746
                                                                                                                                                        CAGCCATCCTCTGGACTTGCTCTGTGACGCTAGCCTCGGGATCCCGCTGTTTTTCCTT
                                                                                                                                                                               GCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGGCTGCGCCTCTTCTCTGT 626
                                                                                                                                                                                                                                          TGAGCAGGTTGTCGGTGTTGACCTGTTGCTCAACTGCTCGCTTCTTCTCTGCCGTGGTGG
                                                                                                                                                                                                                                                                                  TGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTATTGCTGTGCCGCCGGCT 566
                                                                                                                                                                                                                                                                                                                          TGTCCTCCCCTGTGGATCGGGCAATGCGCTAGCTGGGGCCGTGAGCCATCATGGCGGGTT
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Mismatches
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of Use Thereon
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APPLICANT: ALGCE, FROITA.

APPLICANT: MAINTON: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES

FILE REFERENCE: 2077.001200

CURRENT APPLICATION NUMBER: US/09/796.692

CURRENT FAPILICATION NUMBER: 60/186,126

PRIOR APPLICATION NUMBER: 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR APPLICATION NUMBER: 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR APPLICATION NUMBER: 60/200,099

PRIOR APPLICATION NUMBER: 60/200,094

PRIOR APPLICATION NUMBER: 60/202,084

PRIOR APPLICATION NUMBER: 60/202,084

PRIOR APPLICATION NUMBER: 60/202,084

PRIOR APPLICATION NUMBER: 60/202,084

PRIOR FILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: 60/223,416

PRIOR APPLICATION NUMBER: 60/223,416

PRIOR APPLICATION NUMBER: 60/223,378

PRIOR APPLICATION NUMBER: 60/223,378

PRIOR APPLICATION NUMBER: 60/223,378
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      RESULT 11
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; ORGANISM: Homo sapiens
US-09-796-692-2905
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2905
LENGTH: 199
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Publication No. US20020198362A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/223,378 PRIOR FILING DATE: 2000-08-07
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TYPE: DN
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                                                                                                                                                                                                                                                                                                                                                                                                                               1043 CCATGGAGAAGGCAGCATATGGAGTATGAATGCCCCTACTTGGTATATGTGCCCCGTGG 1102
                                                                                                                                                                                                                                                                                                                    1103 TCGCCTTCCGCCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGTGGATGGGGAATTGA 1162
                                                                                                                                                                                                                                       1163 TGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGGATGGTCAGCGGTT 1222
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                                                                                                                                      1223 GCGTGGAGCCCCCGCCCAG 1241
                                                                                  181 GCGTGGAGCCCCCGCCCAG
                                                                                                                                                                                    121 TGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGGATGGTCAGTGGTT 180
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                                                                                                                                                                                                                                                                                           TCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTTGCAGTGGATGGGGAATTGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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 Mismatches

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Pred. No. 1.2e-45;
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                                             RESULT 12
US-10-015-219-658
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Sequence 658, Application US/10015219 Publication No. US20030008299A1
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APPLICANT: Galgar, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Marc
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
TITLE OF INVENTION: UNMER: US,100/040,862
CURRENT FILING DATE: 014058-013520US
CURRENT FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,099
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,094
PRIOR APPLICATION NUMBER: US 60/202,
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; ORGANISM: Homo sapiens
US-10-040-862-2905
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Sequence 2905, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.
SEQ ID NO 2905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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Matches 198; Conservative
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PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
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                                                                                                                                                                                                                                                                                                                                         1103 TCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGTGGATGGGGAATTGA 1162
                                       1223 GCGTGGAGCCCCCGCCCAG 1241
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                                                                                                                                            121 TGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAACTACTTCTGGATGGTCAGTGGTT 180
181 GCGTGGAGCCCCCCCCCAG 199
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Pred. No. 1.2e-45;
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                                       밁
                                                                     QΥ
                                                                                                                                                                               ; NAME/KEY: misc_feature
; LOCATION: (1)...(296)
; OTHER INFORMATION: n = A,T,C or G
US-09-777-564-658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-777-564-658
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 Š
                                                                                                                                                                                                                                                                                                                                                                               Patent NO. COLLEGE GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
TITE REFERENCE: 210121.493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 658
LENGTH: 296
                                                                                                                                                                                                                                                                                                       SEQ ID NO 658
LENGTH: 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 658, Application US/09777564 Patent No. US20020022591A1
                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493C1
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/015,219
CURRENT FILING DATE: 2002-03-02
                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                      1047 GGAGAAGGGCAGGCATATGGAGTATGAATGCCCCCTACTTGGTATATGTGCCCCGTGGTCGC 1106
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1107 CTTCCGCTTGGAGCCCCAAGGATGGGAAAGGTGTGTTTGCAGTGGATGGGGAATTGATGGT 1166
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                                                                                                                             Local Similarity
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les 199; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCCGCTTGGAGCCCAAGGATGGGAAAGGTGTGTTTGCAGTGGATGGGGAATTGATGGT 1166
                                   GAAGAAGGGCAGGCATATGGAGTATGAATGCCCCTACTTGGTATATGTGCCCCGTGGTCGC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGCCCCCCCCAAACCTCGGCCGCAAC 214
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                                                                                                                                                                                                                                                                                                                                              FastSEQ for Window Version 4.0
                                                                                                            Conservative
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                                                                                                                           12.3%;
95.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                          0;
                                                                                                                           Score 193; DB 10; Length 296; Pred. No. 2.2e-44;
                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271, 286,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Farnet, Chris
APPLICANT: Zazopoulos, Emmanuel
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-10-15 NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/976,059
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                                                                                                                                                                                         LOCATION: (13617)...(12802)
OTHER INFORMATION: ORF 9; negative strandedness
NAME/KEY: misc_feature
LOCATION: (15203)...(13614)
OTHER INFORMATION: ORF 10; negative strandedness
NAME/KEY: misc_feature
LOCATION: (19032)..(39713)
OTHER INFORMATION: ORF 13;
                                                            NAME/KEY: misc_feature
LOCATION: (15880)..(19035)
OTHER INFORMATION: ORF 12;
                                                                                                                                                                                                                                                                                                                 LOCATION: (12751). (10829)
OTHER INFORMATION: ORF 8; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COCATION: (9464)..(8130)
OTHER INFORMATION: ORF 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: (9464)..(813)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (7703)..(6693)
OTHER INFORMATION: ORF 5; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COTHER INFORMATION: ORF 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (4038)..(5048) OTHER INFORMATION: ORF 3;
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OTHER INFORMATION: ORF 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (3118)..(4032)
OTHER INFORMATION: ORF 2;
NAME/KEY: misc_feature
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OTHER INFORMATION: ORF 1; positive strandedness
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LOCATION: (2077)..(307)
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                                                                                                                               LOCATION: (15591)..(15863)
OTHER INFORMATION: ORF 11;
                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (9691)..(10761)
OTHER INFORMATION: ORF 7;
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: NAME/KEY: misc_feature
LCCATION: (87494)..(88420)
: OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-09-976-059-1
Вb
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                                                                                                                                                                                       Query Match 2.8%;
Best Local Similarity 45.3%;
Matches 163; Conservative
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LOCATION: (75424). (74213)
OTHER INFORMATION: ORF 22: n
NAME/KEY: misc_feature
LOCATION: (75535). (76464)
OTHER INFORMATION: ORF 23: p
NAME/KEY: misc_feature
LOCATION: (78110). (76449)
OTHER INFORMATION: ORF 24: n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (70659)..(71906)
OTHER INFORMATION: ORF 19; P
NAME/KEY: misc_feature
LOCATION: (73499)..(71964)
OTHER INFORMATION: ORF 20; n
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (84481). (85548)
OTHER INFORMATION: ORF 30; positive strandedness
NAME/KEY: misc_feature
LOCATION: (85556). (86845)
OTHER INFORMATION: ORF 31; positive strandedness
NAME/KEY: misc_feature
LOCATION: (87372). (86803)
OTHER INFORMATION: ORF 32; positive strandedness
OCHER INFORMATION: ORF 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: ORF 15;
NAME/KEY: misc_feature
LOCATION: (66546)...(67370)
OTHER INFORMATION: ORF 16;
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LOCATION: (39713)..(65800)
TOTHER INFORMATION: ORF 14;
NAME/KEY: misc_feature
LOCATION: (65826)..(66530)
                                                                                             16226 GGGCCGTCGCGCAGGTCGCCGGGCCGGTCGAGGGTCGGCCGCCATGCGGCCCAGCGCCGCG 16167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (81524). (79861)
OTHER INFORMATION: ORF 26; negative strandedness
NAME/KEY: misc_feature
LOCATION: (81909). (81682)
OTHER INFORMATION: ORF 27; negative strandedness
NAME/KEY: Misc_feature
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LOCATION: (67384)..(70059)
OTHER INFORMATION: ORF 17;
16166 GCGCGCGGCGCGCGCGCGCGAGGTCCACGACCTGGATCGGGTCGTCGCCGTCCTCG 16107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (74216)..(73563)
OTHER INFORMATION: ORF 21;
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LOCATION: (70099)..(70662)
OTHER INFORMATION: ORF 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (82587)..(84446)
OTHER INFORMATION: ORF 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (82346). (82062)
OTHER INFORMATION: ORF 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (79864).(78107)
OTHER INFORMATION: ORF 25; negative strandedness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAME/KEY: misc_feature
LOCATION: (82346)..(82
                                           95 GGACCCCCTGGCAGCGGGAGCCGGGGTCGAGGTTATGGATCCAGCGGGGGGGCCCCGGG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eature
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CURKERY FILING DATE: 2001-00-13
PRIOR FILLING DATE: 1999-12-14
PRIOR FILLING DATE: 1999-12-14
PRIOR FILLING DATE: 1999-12-27
PRIOR FILLING DATE: 1999-12-29
PRIOR FILLING DATE: 1999-12-29
PRIOR PRIOR PLILING DATE: 1909-12-29
PRIOR PILLING DATE: 2000-01-04
PRIOR PILLING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: 60/174,962
PRIOR FILLING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: 60/223,929
PRIOR FILLING DATE: 2000-08-09
PRIOR FILLING DATE: 2000-08-09
PRIOR FILLING DATE: 2000-08-09
SEDIUNG DE SEDIUNG: 49
SOFTWARE: Patentin Ver. 2.0
CRGANISM: Homo sapiens
FEATURE: NAME WEFF. CDS.
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; LOCATION: (1)..(2898)
US-09-737-149-3
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                                                                                                                                                                                                                                                                                    Query Match 2.8%;
Best Local Similarity 47.3%;
Matches 166; Conservative
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APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-620 CIP
CURRENT APPLICATION NUMBER: US/09/737,149
CURRENT FILING DATE: 2001-06-15
CURRENT FILING DATE: 2001-06-15
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275 GCCAGGCGCTGGTGCCTCCGGGCGTGGCGGCCCTGCTCGCCTTTCCCGAGGCTCGGCCCC 334
                                181 --CTGGTGCTGCTGAACCCGCGCGGCGCCAAGGGCAAGGCCTTGCAGCTCTTCCGGAGTC 238
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Shimkets, Richard A.
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1088.686 Million cell updates/sec
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score greater than or equal S derived by analysis umber of results predicted by chance to have a or equal to the score of the result being printed of the total score distribution.

SUMMARIES

Result No.		Query Match Length DB	ength		ID	Description
ב	2016	100.0	384	21	AAB18659	A human regulator
N		100.0	384	22	AAB93955	Human protein sequ
ω		100.0	384	22	AAB94589	Human protein sequ
4		100.0	384	22	AAE00924	Human sphingosine
υ ₁		99.9	384	22	AAB48007	Human sphingosine
6		99.8	384	22	AAM40180	Human polypeptide
7		99.6	384	23	ABB08089	Human sphingosine
8		99.2	384	21	AAY96057	Human sphingosine
9		97.3	384	22	AAE07882	Human sphingosine
10		86.9	333	23	ABB90209	Human polypeptide

Modified-site Modified-site Modified-site Modified-site Modified-site

/note- 205

181 /note= 137 note-

"potential glycosylation site" "potential phosphorylation site"

Active-site

/note= 54

Location/Qualifiers 16..153

/note= 130

"potential

phosphorylation site"

"potential phosphorylation site"

"diacylglycerol kinase catalytic site"

45	44	43	42	41	40	39	38	37	36	3 5	34	ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; intracellular phosphorylation regulator; HRIP; stroke; myelon neurological disorder; Parkinson's disease; demyelinating disease; meningitis; developmental disorder; neuromuscular disorder; cancer; myasthenia gravis; cell proliferative disorder; actinic keratosis; arteriosclerosis; atherosclerosis; leukaemia; melanoma; bronchitis; arteriosclerosis; atherosclerosis; leukaemia; melanoma; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune disorder; inflammatory disorder; Addison's disease; acquired immunodeficiency disease; allergy; diabetes mellitus; rheumatoid arthritis; microbial infection; trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A human regulator of intracellular phosphorylation
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Best Local S
Matches 384
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20-MAY-1999;
09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human regulator of intracellular phosphorylation (HRIP). HRIP is useful for screening agonists and antagonists of HRIP polypeptide. HRIP and its agonist or antagonist decreased or increased expression of functional HRIP. Diseases treated or diagnosed include neurological disorders such as stroke, Parkinson's disease, demyelinating diseases, bacterial and viral meningitis and other developmental disorders, bacterial and viral meningitis and other developmental disorders of the central nervous system, neuromuscular disorders, myasthenia gravis, cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis and cancer including leukaemia, melanoma, myeloma and cancer of the adrenal gland, bladder, bone, bone marrow, liver, lung, muscle, overy, autoimmune/ inflammatory disorder such as Addison's disease, acquired immunodeficiency disorder such as Addison's disease, acquired immunodeficiency disorder such as Addison's disease, acquired immunodeficiency diseases, altergies, bronchitis, diabetes mellitus, rheumatoid arthritis, microbial infection and trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human intracellular phosphorylation regulator polypeptides and polynucleotides for diagnosis, prevention and treatment of neurological, cell proliferative and autoimmune/inflammatory disorders
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RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFW
                                                  SEKYRRLGEMRETLGTELRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
                                                                                                                                                                                                                                        NHYAGYEQVTNEDLLINCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                                                                                                           SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
                                                                                                                                                                                                    NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
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99US-0135049.
99US-0143188.
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Вþ
                           C? The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary cCC to the complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprises a sequence complementary to the CC complementary strand of a polynucleotide which comprises a sequence complementary to a complementary strand of a polynucleotide which comprises a pend sequence complementary to a CC oligonucleotide comprises a least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence, where the CC oligonucleotide comprises a least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, comprises and be useful for the ccc particularly full-length cDNAs. The primers are also useful for the ccc particularly full-length cDNAs. The primers are also useful for the ccc particularly full-length cDNAs. The primers are also useful for the ccc particularly full-length cDNAs. The primers are also useful for the ccc particularly full-length cDNAs. The primers are also useful for the ccc particularly full-length cDNAs. The primers are also useful for the ccc particularly full-length cDNAs. The primers are also useful for the ccc particularly full-length cDNAs. The primers are also useful for ANH1362B and CC ANH3633 to ANH3642 represent human cDNA sequences; ANB92446 to ANH3632 confidence of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB93955 standard; Protein;
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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, Sugiyama T, Wakamatsu A, Nagai K,
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Query Match

100.0%;

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22;

Length 384

Sequence

384 AA;

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Result
No.
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Listing first 45 summaries
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                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 845.8
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length: 2000000000
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10579.527 Million cell updates/sec
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ALIGNMENTS

RESULT 1 BC014439 LOCUS VERSION KEYWORDS SOURCE ORGANISM DEFINITION ACCESSION COMMENT REFERENCE AUTHORS TITLE REMARK JOURNAL CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcqsc.bc.ca
Steven Jones, Jennifer Asano, Tan Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Strausberg,R.
Direct Submission
Submitted (17-SEP-2001) National Institutes of Health, Mammalian Submitted (17-SEP-2001) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DTP Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2133) Homo sapiens, clone IMAGE:4871343, BC014439 Homo sapiens BC014439.1 GI:17939597 2133 bp mRNA mRNA linear HTC 19-DEC-2001

BG680521

BG680521

Clone distribution: through the I.M.A.G

MGC clone distribution information can be for. E. Consortium/LLNL at: http://image.llnl.gov

George Yang, Scott Zuyderduyn, Marco Marra.

Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Sacedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,

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ORIGIN
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                 GGCTTCGGGGCTGCGCCTCTTCTCTGTGGCCTCAGCCTGGGCCTTCATTGCTGATGT 659
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="MAGE:4871343"
/tissue_type="Skin, melanotic melanoma, high MDR.
/clone_lib="NHH_MGC_49"
/lab_host="Del10B-Rg"
/note="Vector: pOTB7"
a 681 c 719 g 383 t
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ACCESSION VERSION

BM808698 GI:19125509 BM808698.1 GI:19125509 EST. AGENCOURT_6582622 NIH_MGC_41 5', mRNA sequence.

sequence

bp mRNA linear EST 05-MAR-2002 Homo sapiens cDNA clone IMAGE:5471258

KEYWORDS

RESULT 2 BM808698 LOCUS

DEFINITION

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                                                                 TTTGTTCTGAGACCCCCACCCCACGAACCAAATCCAAATAAAGTGACATTCCCAGCCTGA 1559
                                                                                                      TGAAGTCCTGGGTCAGGAGCCCAGCTGGCTGGCCCAGCTGCCTATGTAAGGCCTTCTAG
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                                                                                                                                                          GAGACTCCTCTGGAGAAGGGTGAGAAGGTGGAGGCTATGCTTTGGGGGGGACAGGCCAGAA
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                                                   TTTGTTCTGAGACCCCCACCCACGAACCAAATCCAAATAAAGTGACATTCCCAAAAAAA 2122
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GGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTGCGCAGCCCTGCGCACCTACCGCG
                                                                                                                                          CACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGGCTGCGCCTCTTCTCTGTGCTCA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Tissue Procurement: DCTD/DTP
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National Institutes of Health, Mammalian
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/lab_host="hHl0B (phage=resistant)"
/note="Organ: skin; Vector: poTmp; Site_1: xhoI; Site_2:
/note="Organ: skin; Vector: poTmp; Site_1: xhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5 adaptor:
GCACCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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/db_xref="taxon:9606"
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                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1137)
                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLcM1976 row: f column: 10
High quality sequence stop: 623.
                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                         Unpublished (1999)
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National Institutes of Health, N
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLA
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
Location/Qualifiers
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                                               TCTACGTGCGGGCGGGAGTGTCTCGTGGCATGCTGCTGCGCCTCTTCCTGGCCATGGAGA
                                                                                         TGGGCAGTGAGATGTTTGCTGCACCCATGGGGCCGCTGTGCAGCTTGGCGTCATGCATCTGT 720
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                                                                                                                                                                                        TGGGCAGTGAGATGTTTGCTGCACCCATGGGCCGCTGTGCAGCTGGCGTCATGCATCTGT 991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-*Organ: skin; Voctor: pO/BP; Site_1: xho1; Site_2: EcoRI; cDNA made by ollio-dr prining. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MCC Library.*

342 c 363 g 238 t 6 others
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/clone="IMAGE:5470089"
/clone_lib="NIH_MGC_41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
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96.2%;
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563 GCCTGCTGTCACCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGGGCTGCGCCTCTTCT 622
                                                                                                                                                                                                    443
                                                                                                                                                                                                                                           901 NTTANCGAGGGCCTGGCAGGGCCAAGTGCACCCAAACTACTTC 943
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hes 871;
                                                                                            GCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTATTGCTGTGCCGGC 562
                                                                                                                                                                                   TGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCCTTGAACCATTATGCTG 502
                                                                  GCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTATTGCTGTGCCGCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 892)
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BI860351
BI860351.1 GI:16001098
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_*INAGE:3396178"
/clone_tib=*NHI_MGC_87"
/clone_tib=*NHI_MGC_87"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: breast; Vector: pCMV-SpORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHH MGC Library."
a 266 c 283 g 191 t
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/db_xref="taxon:9606"
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97.3%;
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Pred. No. 2.9e-160;
D; Mismatches 19;
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                                                                                                                                                                                                                                                                                                   AGENCOURT_8414975 NIH_MG
5', mRNA sequence.
BO647377
BQ647377.1 GI:21771549
EST.
          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 888)
                                                                                                                                                                                                                                                                                                                                                                                     BQ647377
                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                CCCCTACTTGGTATATGTGCCCGTGGTCGCCTTCCGCCTTGGAGCCCAAGGATGGGAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                    ACACCTTGTGCCACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGACGA
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                                                                                 TGTGTTTGCAGTGGATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCC
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AAACTACTTCTGGATGGTCAGCGGGTTGCGTGGAGCCCCGCCCCGCCTGGAAGCCCCAG
                                                                TGTGTTTGCAGTGGATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCC
                                                                                                                                  CCCCTACTTGGTATATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGGAAAGG
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/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GCCACGAC(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
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/clone="IMAGE:6272071"
/clone_lib="NIH_MGC_100"
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Pred. No. 1.2e
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L.2e-154;
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RESULT 5 BQ647377

DEFINITION

VERSION ACCESSION

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Matches 781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1314 ACTTGCAGGACCCTTCCTCCTTCCCTAGGGCTGCAGGGCCTGTCCACAGCTCCTGTGGGG 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1255 CAGATGCCACCGCCAGAAGAGCCCTTATGA-CCCCTGGGCCGCGCTGTGCCTTAGTGTCT 1313
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                                                                                                 680 ATCGGCGTCTGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTGGCAGCCCTGC 739
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                                                   TCTCTGTGCCTCACCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAGT 679
                               TCTCTGTGCTCAGCCTGGCCTGGGGCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 785)

NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
BG680521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG680521 785 bp mRNA linear EST 01-MAY-2001 602528344F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4753187 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://image.llnl.gov
Plate: LLAM10612 row
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                               130
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                           /tissue_type="squamous cell carcinoma"
/lab_host="Dil10B (Tl phage resistant)",
/note="Organ: skin: Vector: pcMv-SpORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

231 c 250 g 174 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4753187"
/clone_lib="NCI_CGAP_Skn4"
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Pred. No. 1.4e-143;
0; Mismatches 2;
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 AI769914 772 bp mrNA linear EST 21-DEC-1999 wj30d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2404331 3' similar to TR:088886 088886 SPHINGOSINE KINASE.;, mrNA sequence.
                                                                                                                                                             Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 772)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                           Emmert-Buck, M.D., Ph.D.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:2404331"
/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
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AGENCOURT_6641989 NIH_MGC_41
5', mRNA sequence
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Tissue Procurement: DCTD/DTP
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National Institutes of Health, M
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BM916526
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Location/Qualifiers
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http://image.llnl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/clone_lib="NIH_MGC_41"
/tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTH7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: poTH7; Site_2: XhoI; Site_1: XhoI; Site_1: XhoI; Site_1: XhoI; Site_1: XhoI; Site_2: XhoI; Site_1: XhoI;
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/db_xref="taxon:9606"
/clone="IMAGE:5482958"
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Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200.element cDNA microarray Unpublished (2000)
Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 3528 Email: Johnq@tigr.org
                                                                                                                                                                                                                                                                                                                                                               AWY05415 '676 bp mRNA linear EST 01-JUN-200 EST375488 MAGE resequences, MAGH Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 676)
                                                                                                                                                                                              Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
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                                                                                              BE464487 702 bp mrNA linear EST 27-JUL-2000 hz17g10.xl NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3208290 3' similar to TR:088886 OB8886 SPHINGOSINE KINASE.;, mRNA sequence.
            Homo sapiens
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/db_xref-"taxon:9606"
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/notce-"Vector: pBluescriptSkm"
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TITLE AUTHORS

> Quackenbush, J. Hegde, P.,

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                                                                                                                                              GGGAATTGATGGTTAGCGAGGCCGTGCAGGGCCAGGTGCACCCAAACTACTTCTGGATGG
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                                                            TCAGCGGTTGCGTGGAGCCCCCGCCAGCTGGAAGCCCCAGCAGATGCCACCGCCAGAAG
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AGCCCTTATGACCCCTGGGCCGCGCTGTGCCTTAGTGTCTACTTGCAGGACCCTTCCTCC 1333
                                                                                                                          GGGAATTGATGGTTAGCGAGCCCGTGCAGGGCCAGGTGCACCCCAAACTACTTCTGGATGG
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Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 454.
Location/Qualifiers
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DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
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National Cancer Institute, Cancer Genome Ana
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1 (bases 1 to 702)
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/db_xref="taxon:9606"
/clone="IMAGE:3208290"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stenford)
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 875)
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                       Similarity
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    Conservative
                                                                                                  1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

a 252 c 272 g 192 t
                                                                                                                                                                                                                          /tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: Xho1; Site_2:
EcoR1; cDNA made by oligo-dT priming. Directionally cloned
into EcoR1/Xho1 sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5433632"
/clone_lib="NIH_MGC_100"
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  NIH-MGC
                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 793)
                                                                                                                                                                    mRNA sequence.
BG678689
                                                                                                                                                                                                     BG678689 793. bp mRNA linear EST 01-MAY-2001 602624488F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4749573 5',
                                                                                     Homo sapiens
                                                                                                                                                 BG678689.1
  http://mgc.nci.nih.gov/
                                                                                                                                                 GI:13910086
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CCCTCTCACTGGACAGTGGTGCCCGACGAGGACT-TTGTGCTAGTCCTGGCACTGCTGCA
                                                                                                                                                                 GCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGGGTTCCAAGACACCTG--CCTCCCC
                                                                                                                                                                                                          TGGGGGAGATGCGCTTCACTCTGGGCACCTTCCTGCGTCTGGCAGCCTGCGCACCTACC
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.goy
Ilssue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://image.llnl.gov
Plate: LLAM10602 row: p column: 22
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Skn4"
/clone_lib="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sali; Cloned unidirectionally primer: Oligo dT.
Ste_2: Sali; Cloned unidirectionally constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 244 c 255 g 165 t
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93.8%;
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Pred. No. 1.8e-121;
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BW386957
BW386957.1 GI:18187010
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: msoares@blue.weeg.ulowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail.cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact:
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                         salivary gland. It was constructed according to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 791-806, 1996). For construction of the CNI library, plasmid DNA from the pool of normalized libraries was electroporated into competent bacteria for the production of single-stranded circular DNA. This was then used as a tracer in a subtractive hybridization with
                                                                                                                                                                                                                                                                                                                /lab_host="DH10B [Life Technologies]"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CN1
library is a subtracted library derived from the following
pool of seven normalized rat libraries: normalized rat
seminal vesicles, normalized rat penis, normalized rat
bladder, normalized rat fundus, and normalized rat
madipose, normalized rat fundus, and normalized rat
religious products of the control of the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="UI-R-CN1-cji-c-13-0-UI"
/clone_lib="UI-R-CN1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
driver (PCR amplified inserts from a plamid DNA template
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preparation) comprising; a) a pool of about 34,000 clones from the Rat Unigene Set corresponding to plates R-5-An NN of the final driver population. b) a pool of about 29,000 clones from subtracted libraries CAO and CAI corresponding to plates R-5-An NN of the final driver population. b) a pool of about 29,000 clones from subtracted libraries CAO and CAI corresponding to plates R-CAO-MSE through R-CAO-MSE K-CAO-MSE through R-CAO-MSE K-CAO-MSE Through R-CAO-MSE R-CAO-MSE R-CAO-M

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RESULT 14
-AI972156/6
-LOCUS
DEFINITION
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AUTHORS
TITLE
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VERSION
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 AGGGTGAGAAGGTGGAGGCTATGCTTTGGGGGGACAGGCCAGAATGAAGTCCTGGGTCAG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTAGGGCTGCAGGGCCTGTCCACAGCTCCTGTGGGGGGTGGAGGAGACTCCTCTGGAGA 1395
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638 bp mRNA linear EST 08-MAR-2000 wr63c05.x1 NCI_CGAP_Utl Homo sapiens cDNA clone IMAGE:2492360 3' similar to TR:088886 O88886 SPHINGOSINE KINASE.;, mRNA sequence.
Tumor Gene Index.
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: egapbs r@mail.nih.gov
Email: egapbs r@mail.christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalla; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 638) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                         Homo sapiens
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Pred. No. 1.1e-120;
0; Mismatches 11; Indels 1;
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Query Match
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                                                                        1519 CCCACGAACCAAATCCAAATAAAGTGACATTCCCA 1553
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                                                                                                                                                                                                                                                                                                             398 TTGATGGTTAGCGAGGCCGTGCAGGCCCAGGTGCACCCCAAACTACTTCTGGATGCTCAGC 339
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38 CCCACGAACCAAATCCAAATAAAGTGACATTCCCA 4
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CDNA Library Arrayed by: Greg Lemnon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: WCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortlum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1774 Std Error: 0.00
Seq primer: -40UP from Gibbo
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Location/Qualifiers
1. .638
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/db_xref="taxon:9606"
/clone="IMAGE:2492360"
/clone=Lib="NCI_CGAP_Utl"
/tissue_type-"well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014," 175 g 119 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.5%;
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Pred. No. 5.5e-120;
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VERSION
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TITLE
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Best Local
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AAGGATGGGAAAGGTGTGTTTGCAGTGGATGGGGAATTGATGGTTAGCGAGGCCGTGCAG
                                                                                                                                                                                                                                                                                       GTGCCCGACGAGGACTTTGTGCTAGTCCTGGCACTGCTGCACTCGCACCTGGGCAGTGAG 942
                                                                                                                                                                                                                                                                                                                                                             GGCCCGGTAGATGCACACCTTGTGCCACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTG 882
                                                                                          ATGGAGTATGAATGCCCCTACTTGGTATATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCC
                                                                                                                                                               ATGGAGTATGAATGCCCCTACTTGGTATACGTGCCCGTGGTCGCCTTCCGCTTGGAGCCC
                                                                                                                                              ATGTTTGCTGCACCCATGGGCCGCTGTGCAGCTGGCGTCATGCATCTGTTCTACGTGCGG 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG280830 809 bp mRNA linear EST 21-FEB-2001 602401209Fl NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4543395 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM1225 row: b column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 809)
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BG280830
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Clone in Industrial MCC_20"
/clone_libe "NHI_MCC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="Directionally cloned into EcoRI/XhoI sites using the following 5'
adaptor: GCCACGACGO. Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
California, Berkeley) using ZAP-cDNA synthesis kit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref*"taxon:9606"
/clone="IMAGE:4543395"
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727
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                                                          -GCTGCCTATGTAAGGCCTTCTAG-TTTGTTCTGAGACC-CCCACCCCCACGAACCAAATC
                                                                                             CTTTG-GGGGGACAGGCCA-GAATGAAGTCCTGGGTCAGGAGCCCAGCTGGCTGGCCCA 1476
                                                                                                                                             CTCCTGTGGGGGTGGCAGGAGACTCCTCTGGCACAAGGGTGAGAAGGTCGGCAGGCTATG
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                                                                                                                                                                                                                                          CAAATAAAGTGAACATTCCA
                                              GGCTGCCTATGTAAGGCCTTCTAGCTTCGTTCTGAGACCACACAGCCCACGAACCAAATC
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Search completed: May 17, 2003, 14:17:36
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Match
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2016
1 MDPAGGPRGVLPRPO
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sp_unclassified:*
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 Q9VZW0
Q8T0C1
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Q8T269
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Q9H0Q2
Q9BRN1
Q9D4D1
Q9VYY8
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Q96GK1
Q9NOA5
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Q88886
Q88885
Q91V26
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Q9vyy8 drosophila
Q9vzw0 drosophila
Q8t0c1 drosophila
O65419 arabidopsis
Q8t269 dictyosteli
                                                                                                     096hv8 homo sapien
096gX1 homo sapien
09n0a5 macaca fasc
091zn3 mus musculu
088886 mus musculu
088885 mus musculu
091v26 rattus norv
                                                        Q9btg7 homo sapien
Q9h0q2 homo sapien
Q9brn1 homo sapien
Q9d4d1 mus musculu
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125	126	127	129.5	130	131	136.5	140.5	140.5	148	155.5	162.5	185	203	213.5		239	239	250	250.5	264.5	264.5	265	272	345	355	356.5	363.5	374.5
6.2	6.2	6.3	6.4			6.8			7.3	7.7	8.1	9.2	10.1	10.6	11.3	11.9	11.9	12.4	12.4	13.1	13.1	13.1	13.5	•				18.6
340	302	342	303	295	586	309	338	306	173	306	406	533	421	422	326	596	487	732	549	537	481	757	763	624	458	687	354	473
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Q9A0J4	Q9CEN8	Q9CIE3	031502	Q9KBH4	Q949C3	034799	Q94C71	Q8Y497	Q9D087	Q927T6	Q9VL10	Q9LU45	Q9ESW4	Q9NP48	Q9UGE5	Q9VNA6	Q95S15	Q9FHL3	Q9TZI1	Q8TCT0	Q9BYB3	Q94HY9	Q9LRB0	Q12246	014159	Q06147	Q9NWU7	Q18425
Q9a0j4 streptococc	Q9cen8 lactococcus	Q9cie3 lactococcus	O31502 bacillus su		Q949c3 oryza sativ		Q94c71 arabidopsis	Q8y497 listeria mo			a.	Q9lu45 arabidopsis	4 mus		Q9uge5 homo sapien		Q95s15 drosophila	(4)		Q8tct0 homo sapien			0		014159 schizosacch		Q9nwu7 homo sapien	Q18425 caenorhabdi

ALIGNMENTS

Qγ	DЪ	Qy	Db	QY	Qu. Be.	QS	DR DR	DR	DR	DR	DR	DR	RĽ	RA	RC	RP	RN	2	8	8	SO	DE	TO	TO	DT	Ac	H	RESULT
121 NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180	61 RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120	61 RELVRSEELGRWDALVYMSGDGLMHEVVNGLMERPDWETAIOKPLCSLPAGSGNALAASL 120	1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA 60	1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA 60	Query Match 99.7%; Score 2009; DB 4; Length 384; Best Local Similarity 99.7%; Pred. No. 5e-168; Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		ProDom; PD005043; DAG_kin_cat; 1. PROSITE: PS00063: ALDOKETO REDUCTASE 3: UNKNOWN 1	Pfam; PF00781; DAGKC; 1		InterPro; IPR001206; DAGKC.	InterPro; IPR001395; Aldo/ket_red.	08040; AAH08040.1;	Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.	Strausberg R.;	TISSUE=SKIN;	SEQUENCE FROM N.A.	[1]		Primates; Catarrhini; Hominidae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	Unknown (protein for MGC:15041).	20,	(TrEMBLrel. 19,	2001 (TrEMBLrel.		Q96HV8 PRELIMINARY; PRT; 384 AA.	/パ /8

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Query Match
Best Local :
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Q96GK1;
Q96GK1;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:15040).
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: 1...
Pfam; PF00781; DAGKC; 1.
ProDom; PD00784; DAG_Kin_Gat; 1.
ProDom; PD005043; DAG_Kin_Gat; 1.
PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC009419; AAH09419.1; -.
InterPro; IPR001395; Aldo/ket_red.
InterPro; IPR00156; DAKC.
InterPro; IPR003622; DAG_kin_cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-KIDNEY;
                                        287 LFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-9606;
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       301 LFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMV
                                                                                  241 VVVQQGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMH
                                                                                                                                                                  181
                                                                                                                                                                                     167 LSLAWGFIADVDLESEKYRRLGEMRETLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASP 226
                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                   107 SLPAGSGNALAASLNHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSV 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 LEEPVPSHWTVVPDEDFYLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL
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                                                                                                                                                                                                                                                                                                                                                                                                              1 MDPVVGCGRGLEGEVESAGGPRGVLPRPCRVLVLLNPRGGKGKALQLERSHVQPLLAEAE 60
                                                                                                                                                                  LSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVVQQGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMH 286
                                                                                                                                                                                                                                              SLPAGSGNALAASLNHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSY, 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.2%; Score 1999; DB 4; Length 398; ilarity 96.5%; Pred. No. 3.9e-167; Conservative 0; Mismatches 0; Indels 14; Gaps
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Best Local
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091ZN3 PRELIMINARY; PRT; 381 AA.
091ZN3; 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seguence update)
01-DUN-2002 (TrEMBLrel. 21, Last annotation updat sphingosine kinase 1a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09NOA5;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Unnamed protein product.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
NCBI_TaxID-9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prodom; PD005043; DAG_kin_cat; 1.
SMART; SM00046; DAGKC; 1.
PROSSTTE; PS000063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
SEQUENCE 329 AA; 36393 MW; 7F430ABDOCASFDC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       libraries.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL. AB046025; BAB01607.1;
InterPro; IPR001395; Aldo/ket_red.
InterPro; IPR001206; DAGKC.
InterPro; IPR001226; DAGKC.
InterPro; IPR00322; DAG_kin_cat.
Pfam; PF00781; DAGKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09N0A5
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                                                                                                                                                                                                                                                                                                                                                                                           181 SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
                                                                                                                                                                                                                                                                                                                241 LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300
                                                                                                                                                                                                                                                                                                                                                                      181 SEKYRRLGEMRETLGTELRLAALRTYRGRLAYLPYGRAGSKTPVSPVVVQQGPVDAHLVP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NHYAGYEQVTNEDLLTNCTRLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                                        301 RLFLAMEKGRHMEYECPYLVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 81.5%; Score 1644; DB 6; Length 329; Similarity 98.1%; Pred. No. 4.4e-136;
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                                     sphingosine kinase.";
J. Biol. Chem. 273:23722-23728(1998).
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Sphingosine kinase (Fragment).
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"Molecular cloning and functional cha
sphingosine kinase.";
J. Biol. Chem. 273:23722-23728(1998).
EMBL; AF068748; AAC61697.1; -.
MGD; MGI:1316649; Sphk1.
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MEDLINE-98395082; PubMed-9726979;
MEDLINE-98395082; PubMed-9726979;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKc; 1.
DAG_kin_cat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43254 MW;
  55119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.9%;
81.7%;
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DAG_kin_cat.
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  MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1630.5; DB 11; Length Pred. No. 8.3e-135; Pred. No. 8.3e-135; Indels 2; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01EB032322542CAD CRC64;
2AAFEBA72027F509 CRC64;
                                                                                                                                                                                                                                                       Nagiec M.M., Dick characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
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                                                                                                                                                                                                                                                           murine
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Query Match

80.7%;

Score 1627.5;

DB

Length

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91V26
1D 091V
AC 091V
DT 01-M
DT 01-M
DE Sphi
DE Sphi
DE SPK
CO Euka
OC Buka
OC Mamma
OX NCBI
RN [1]
RP SEQU
RA STAC
OX MCBI
RN [1]
RP SEQU
RE BUBL
DR EMBL
DR Inte
DR FAMB
DR PFOD
DR WKIAB
DR FEBOUR
DR FEBOUR
DR EMBL
DR EM
                                                                                                                                                                                                      Matches 300;
                                                                                                                                                                                                                                                 Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q91V26 PRELIMINARY; PRT; 383 AA.
Q91V26;
Q91V26;
Q91V26;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Sphingosine kinase 1f (Sphingosine kinase la) (Sphingosine kinase la)
(Sphingosine kinase 1d) (Sphingosine kinase le).
SPHKIF OR SPHKIC OR SPHKIC OR SPHKIE OR SPHKIE.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shiota K.;

CGG island of rat sphingosine kinase-1 gene: tissue-dependent DNA methylation status and multiple alternative first exons.";

Genomics 78:117-125(2001).

EMBL: AB049575: BAB62324.1; -.

EMBL: AB049571: BAB6232.1: -.

EMBL: AB049572: BAB6232.1; -.

EMBL: AB049573: BAB6232.1; -.

EMBL: AB049573: BAB6232.1; -.

EMBL: AB049574: BAB6232.1; -.

EMBL: AB049578: BAB6232.1; -.

EMBL: AB049579: BAB
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD005043; DAG_kin_cat; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mamura T., Ohgane J., Ito S., Ogawa T., Hattori N., Tanaka
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                                     1 MQPADCPRGLLPRPCRVLVLLNPRGGKGKALKLFQSRVRPLLEEAEVSFKLMLTERQNHA 60
                                                                                                                      1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVDGOVHPNYFWMVSGCV 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGEMRETLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EELGHWDALAVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPGGSGNALAASVNHYAGY 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRGELPRPCRVLVLLNPQGGKGKALQLFQSRVQPFLEEAEITFKLILTERKNHARELVCA 188
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307; Conserv
                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                              383 AA; 42418 MW; CAAD5817BF4B9507 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                   79.3%; Score 1599.5; DB 1
78.1%; Pred. No. 4.3e-132;
                                                                                                                                                                                                  42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Mismatches
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3; Mismatches 36;
                                                                                                                                                                                                                                                                             DB 11; Length 383;
                                                                                                                                                                                                  41; Indels
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similar to sphingosine kinase 1 (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC004112; AAH04112.1; -.
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                                                                                                                                                                 338 FAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL 384
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                                                                                                                      244 FAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSWKPQOMPPPEEPL 290
                                                                                                                                                                                                                                                                                  184 GRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGV
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287; Conserv
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Q9HQQ2;
Q1-MAR-2001
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HOMO Sapiens (Human).
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ProDom; PD005043; DAG_kin_cat; 1.
SMART; SM00046; DAGKC; 1.
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"Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U1-MAR-2001 (TrEMBLrel. 16, Cr. 01-MAR-2001 (TrEMBLrel. 16, La. 01-DEC-2001 (TrEMBLrel. 19, La. Hypothetical 69.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein SEQUENCE 654 AA;
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EMBL; AL136701; CAB66636.1; -.
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Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
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InterPro; IPR003622; DAG_kin_cat.
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                                                                                                                    EGDFVLMLAISPSHLGADLVAAPHARFDDGLVHLCWVRSGISRAALLRLFLAMERGSHFS
                                                                                                                                                                              GSPKAALHSPVSEGAPVIPPSSGLPLPTPDARVGASTCGPPDHLLPPLGTPLPPDW-VTL
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                                                          LGCPQLGYAAARAFRLEPLTPRGVLTVDGEQVEYGPLQAQMHPGIGTLLTG---
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ilarity 39.8%;
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Pred. No. 3.1e-69;
1; Mismatches 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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01-JUN-2001 (TrEMBLrel. 17, Last sequence upon the control of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00046; DAGKC; 1.
Hypothetical protein.
SEQUENCE 654 AA; 69217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC006161; AAH06161.1; -. InterPro; IPR001206; DAGKC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9BRN1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9BRN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003622; DAG_kin_cat.
Pfam; PF00781; DAGKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD005043; DAG_kin_cat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-LYMPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
650
                                                     374
                                                                                                                                                                                                                                                                                                                                              476
                                                                                                                                                                                                                                                                                                                                                                                                                                                            416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
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                                                                                                                                                           YECPYLYYYPYVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSWK 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRFTLGTFLRLAALRTYRGRLAYLPVG-RVGSKTPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGLDLLLLNCSLLLCRGGGHPLDLLSVTLASGSRCFSFLSVAWGFVSDVDIQSERFRALGS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THEOLITHCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQV 129
                                                  PQQMPPPEEP
                                                                                                           LGCPQLGYAAARAFRLEPLTPRGVLTVDGEQVEYGPLQAQMHPGIGTLLTG----PPGC- 649
                                                                                                                                                                                                                            EGDFVLMLAISPSHLGADLVAAPHARFDDGLVHLCWVRSGISRAALLRLFLAMERGSHFS
                                                                                                                                                                                                                                                                               DEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHME 313
                                                                                                                                                                                                                                                                                                                                           GSPKAALHSPVSEGAPVIPPSSGLPLPTPDARVGASTCGPPDHLLPPLGTPLPPDW-VTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LHRSVSDLPLPLPQPALASPGSPEPLPILSLNGGGPELAGDWGGAGDAPLSPDPLLSSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARFTLGTVLGLATLHTYRGRLSYLPATVEPASPTPAHSLPRAKSELTLTPDPAPPMAHSP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEWDGIVTVSGDGLLHEVLNGLLDRPDWEEAVKMPVGILPCGSGNALAGAVNQHGGFEPA
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----PGREP
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654
                                                     383
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                SPVVVQQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69217 MW; F73FFCEC930DA50F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.0%;
39.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 886.5; DB 4
Pred. No. 3.1e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 107; Indels 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               654
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6

RESULT 11 Q9D4D1

PAC

Q9D4D1 Q9D4D1; 01-JUN-2001

PRELIMINARY;

17,

Created)

PRT;

384 AA

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RESULT 12
Q9VYY8
ID Q9VYY
AC Q9VYY
DT 01-MA
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RM MEDLINE-21085660; PubMed-11217851;

RA ARAWA T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Arakawa T., Hara A., Shibata K., Yoshino M., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R., RA Aizawa K., Matsuda H.A., Ashburner M., Batahov S., Casavant T., RA Kadota K., Matsuda H.A., Ashburner M., Batahov S., Casavant T., RA RA Leischmann W., Gaasterland T., Glasi C., King B., Kochiwa H., Ra Ra Pleischmann W., Gasaterland T., Glasi C., King B., Kochiwa H., Wagner L., Washio T., RA RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Sakai K., Okido T., Furuno M., Aono H., Baldareili R., Barsh G., RA Sakai K., Okido T., Furuno M., Aono H., Baldareili R., Barsh G., RA Sakai K., Okido T., Furuno M., Aono H., Baldareili R., Barsh G., RA Sakai K., Okido T., Furuno M., Aono H., Baldareili R., Barsh G., RA Sakai K., Okido T., Furuno M., Aono H., Baldareili R., Barsh G., RA Sakai K., Okido T., Furuno M., Aono H., Baldareili R., Barsh G., RA Sakai K., Hill D., Hofmann M., Hune D., Kamiya M., Lee N.H., RA Lyons P., Marchhonni L., Mashima J., Mazzareili J., Mombaerts P., RA Sasaki H., Toyo-oka K., Wang K.H., Waitz C., Whihatake C., Whining L., RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S., RA Havashtzaki Y., Scholaka, Haseshtzaki Y., Scholaka, Kana Marashtzaki Y., Scholaka, Haseshtzaki Y., Scholaka, Haseshtzaki Y., Scholaka, Haseshtzaki Y., Scholak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
   Q9VYY8;
01-maY-2000 (TrEMBLrel. 13, Created)
                                                       BAAA60
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Ol-MAR-2002 (TERMILTEL 20, Last annotation update)
Adult male testis CDNA, RIKEN full-length enriched library,
Clone:4933402E20, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-10090;
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                                                                                                                                                                                             361 PIQAQVHPGLATLLTG----PAGQKPQ 383
                                                                                                                                                                                                                                                  349 AVQGQVHPNYFWMVSGCVEPPPSWKPQ 375
                                                                                                                                                                                                                                                                                                      301 WVRSGISRAALLRILLAMEHGNHFSLGCPHLGYAAARAFRLEPLTPRGLLTVDGELVEYG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 GPELTGDWGGAGDAPLSPDPLLPSSPNALKTAQLSPIAEGPPEMPASSGFLPPTHSAPEA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 PLCSLPAGSGNALAASLNHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRL 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQQGPVDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLF 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGHSLPRAKSELVLAPAPAPAATHSPLHRSVSDLPLPLPQPALVSPGSPEPLPDLSLNGG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSVLSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPV----- 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIGVLPCGSGNALLGAVNHHGGFEQVVGVDLLLNCSLLLCRGGSHPLDLLSVTLASGSRC 61
                                                                                                                                                                                                                                                                                                                                                        YVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSE 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSFLSVAWGFLSDVDIHSERFRALGSARFTLGAVLGLASLHTYRGRLSYLPATTEPALPI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AK016616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  вав30339.1;
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Pred. No. 4
                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                          641 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 384;
.3e-45;
es 88; Indels 120;
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126 -YEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLR---LFSVLSLAWGFIADVDLES 181
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RX MEDLINE-2019606; PubMed-10731132;
RA Adams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe W., Pfeiffer B.D.,
RA Baradon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Apbayani A., An H.-J., Andrews Pfannkoch C. Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktargulu L., Beasley E.M.,
RA Beeson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies S.,
RA Godek C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Godek C., Garrell J.H., Gu Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunkov B.C., Dlann P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Mattel B., Kelntosh T.C., Kez Y., Kenison J.A., Ketchum K.A.,
RA Harris N., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
RA Harris N., Wattel B., Kelntosh T.C., McLeod M.P., Mehreson D.L.,
RA Hasko P., Lei Y., Levitsky A.A., Li J., Li Z., Llang Y., Lin X.,
RA Hashilov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA McMillov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Hashilov G., Staplenco N., Skupletton M., Skupski N.P., Smith T.,
RA Hashilov B.C., Staplenco N., Skupletton M., Skupski N.P., Smith T.,
RA Spier E., Spradling A.C., Stapletton M., Skupski N.P., Smith T.,
RA Shen S.H., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Shen S.H., Woodage T., 
                                                                                                                                                                                                                                                                                 InterPro; IPR001206; DAGKC.
InterPro; IPR001622; DAG_Kin_cat.
Pfam; PF00781; DAGC; 1.
Probom; PD005043; DAG_Kin_cat; 1.
SMART; SM00046; DAGKc; 1.
SEQUENCE 641 AA; 71421 MW; 1CE24E4BDF14758D CRC64;
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Eukaryota: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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244 LLTRYSGIVVASGDGLFYEVLNGLMERMDWRRACRELPLGIIPCGSGNGLAKSVAHHCNE 303
                                                                                                 184 PADCGKQLLILLNPKSGSGKGRELFOKQVAPLLTEAEVQYDLQITTHPQYAKEFVRTRRD 243
                                                                                                                                              12 PRPC--RVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEE- 68
                                                                                                                                                                                                                       Local Similarity
                                                  -LGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQK-PLCSLPAGSGNALAASLNHYAG- 125
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                    27.9%; Score 562; DB 5; Length 641; 32.5%; Pred. No. 9.1e-41;
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                                                                                                                                                                                              67; Mismatches 121; Indels 120;
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RESOLUTION OF THE PROPERTY OF 
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01-MAY-2000
01-OCT-2001
CG2159 prote
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL; AE003476; AE747706.1; -.
FlyBase; FBgn0035391; Ccorr
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SMART; SM00046; DAGKC; 1.
SMART; SM00516; SEC14; 1.
SEQUENCE 907 AA; 102561 MW;
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Pfam; PF00781; DAGKC; 1.
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628
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                            VFAVDGELMVSEAVQGQVHP
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                                                                                                                                                                                                                                                                                                                                                                                                                           RVLVLLNPKSGSGDAREVENMHVTPVLNEAEVPYDLYVTKHSNFAIEFLSTRCLDAWCCV
IITVDGERVEFGPLQAEVLP
                                                                                      GRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHM-EYECPYLVYVPVVAFRLEPKDGKG
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                                                          AQLNDGTIYLILIRAGISRPHLLSFLYNMSSGTHLPESHDDHVKVLPVRAFRLEPYDNHG
                                                                                                                    GLAAASLENRQQNYGPASELPDLNEPLSEDQGWLVEEGEFVMMHAVYQTHLGIDCHFAPK
                                                                                                                                                                                                                                          WTLYRLVNLRTYNGRISYLLTDHEVSSTHSATGYAAQRRMQSSRSCNTHIDMLNGPAPIY 447
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Similarity 30.5%;
34; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAG_kin_cat.
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647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 521.5; DB 5; pred. No. 5.1e-37; 61; Mismatches 138;
                                                                                                                                                  -----VVPDEDFVLVLALLHSHLGSEMFAAPM
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RESULT
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AC QRESULT
DT 000
DT 
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Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                    Ephydroidea; Drosophilidae; NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila
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           STRAIN-BERKELEY
                                                          SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster (Fruit fly)
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21,
21,
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Last annotation update)
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ı; Brachycera;
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Muscomorpha;

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RESULT 15
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06541
ID 06541
AC 06541
DT 01-AU
DT 01-AU
DT 01-AU
DT 01-OE
GN F1BE5
OS Arable
OC Eukar
OC Sperm
OC SPERM
OC NCBL;
RN [1]
RN [1]
RN [2]
RN [2]
RN [2]
RN SEQUE
RA Bevan
RA Submit
RN SEQUE
RA SUBMIT
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Matches 133; Conserv
                                                                                                                                                                                                                                                                                                    Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY069417; AML395621; -
EMBL, AY069417; AML395621; -
EMBL/GenBank/DDBJ GRC664;
                                                                                                                                                                                      SEQUENCE FROM N.A.

Bevan M., Peters S.A:, van Staveren M., Dirkse W., Stiekema Bancroft I., Mewes H.W., Mayer K., Schueller C.;

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                            Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                         SEQUENCE FROM N.A. Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W., Lemeke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702
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                                           EQUENCE FROM N.A.
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Arabidopsis sequencing project;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQLNDGTIYLILIRAGISRPHLLSFLYNMSSGTHLPESHDDHVKVLPVRAFRLEPYDNHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLAAASLENRQQNYGPASELPDLNEPLSEDQGWLVEEGEFVMMHAVYQTHLGIDCHFAPK 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEMRFTL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVMSGDGLMHEVVNGLMERPDWETAI-QKPLCSLPAGSGNALAASLNHYAGYEQVTNEDL 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. SEQUENCE 1240 AA;
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711 EPGALVDEPDKEGIIDSDGEVL 732
                                                                                     654 APAAKFSDGYLDLIVLK-NCPKLVLLSLMRQTSSGTHV--ESPYIVYIKLTVEKVKAFVL 710
                                                                                                                                                                                                                                                           548 RIDEYVCLVDKFDNYCIAVVKLLALQRIICLRRYNGRILFLPAPGFEGYGQPASCSLYQE 607
                                                                                                                                                                                                                                                                                                                                                                                                                                          434 KYDGIVCVSGDGILVEVVNGLLERADWRNALKLPIGMVPAGTGNGMIKSLLDTVGLRCCA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 LGRPKRLLVFVNPFGGKKSAREIFVKEVKPLFEDADVQLEIQETKYQLHAKEFVKSMDVS 433
                                        330 EP-----KDGKGVFAVDGELM 345
                                                                                                                           275 APMGRCAAGVMHLEYVRAGVSRAMLLRLELAMEKGRHMEYECPYLVYV-----PVVAFRL 329
                                                                                                                                                                        608 PHVSDKEVGYQGPETKFEDLEWREMKGPFVTIW-------LHNVPWGSENTLT 653
                                                                                                                                                                                                                 231 ------QGP----VDAHLVPLEEPVPSHWTVVPDEDFVLVLALLHS-HLGSE-MFA 274
                                                                                                                                                                                                                                                                                                         191 RFTLGTFL------RLAALRTYRGRLAYLPV-GRVGSKTPASPVVVQ- 230
                                                                                                                                                                                                                                                                                                                                               494 N----SATISTIRGHKRSVDVATI-AQGNTKFFSVLMLAWGLIADIDIESEKFRWMGSA 547
                                                                                                                                                                                                                                                                                                                                                                                         131 NEDLLINCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEM 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 RWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVT 130
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122; Conservative
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13;

Search completed: May 9, 2003, 16:56:56 Job time: 95 secs

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1573
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1428.4 90.8 1438 22 AAI5936 Human 1168.6 74.1 1173 22 AAC84161 Human 1165.74.1 1173 24 ABL59522 Human 1163.2 73.9 1200 22 AAI61122 MOUSE 853.2 54.2 1759 22 AAI6445 Human 387.6 24.6 394 24 ABL66446 Human 387.6 22.4 AAI 675 22 AAH107214 Human 262.8 16.7 2380 24 AAI67214 Human 262.8 16.7 2422 23 AAAI6443 Human 262.8 16.7 2422 23 AASS331 Human 262.8 16.7 2422 23 AASS331 Human 188.2 12.0 2136 22 AAR9477 Human 188.2 12.0 2136 22 AAR9477 Human 116.5 7.4 1521 22 AAD9234 Human 112.8 7.2 1394 24 ABL5923 Human 112.8 7.2 1394 24 ABC5330 Human 112.8 7.2 1394 24 ABC3327 Drosop 91.4 5.8 4020 23 ABL02327 Drosop Drosop Drosop Drosop Drosop Drosop Drosop Drosop Drosop Human Human Human 151.2 3.3 423.3 274 ABC9650 Human Human Human Human 151.2 3.3 423.3 274 ABC9650 Human Human Human 151.2 3.3 423.3 274 ABC9650 Human Human Human Human 151.2 3.3 423.3 274 ABC9650 Human Human Human Human 151.2 3.3 423.3 274 ABC9650 Human Human Human Human Human 151.2 3.3 423.3 274 ABC9650 Human Human Human Human Human 151.2 3.3 423.3 274 ABC9650 Human Hu	Human sphingosine	ABL40828	24	4413		51.2	4. 1	
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1428.4 90.8 1438 22 AAC15936 Human poly 1168.5 74.3 1205 22 AAC84161 Human sphil 1163.5 74.1 1173 24 ABL59532 Human sphil 1163.2 73.9 1200 22 AAD147167 Human sphil 1163.2 73.9 1200 22 AAD14475 Human poly 853.4 54.2 175.9 22 AAD14475 Mouse sphil 853.2 54.2 175.9 22 AAD1445 Mouse sphil 510.2 32.4 687.9 22 AAD1445 Mouse sphil 510.2 32.4 675.2 22 AAD1445 Human cDNA 387.6 24.6 675.2 23 AAH07214 Human cDNA 389.6 23.3 4 675.2 23 AAH0443 Lung cance 389.6 23.4 481.593 23 AAH0443 Human cDNA 319.6 16.7 2380 2	Drosophila melanog	ABL03296	23	4020		91.4	38	
1428.4 90.8 1438 22 AAC15936 Human poly 1168.5 74.3 1205 22 AAC84161 Human sphi 1165.5 74.1 1173 24 ABL59532 Human sphi 1163.2 73.9 1200 22 AAD161122 Human poly 853.2 54.2 1759 22 AAD14465 Mouse sphi 853.2 54.2 1759 22 AAD14425 Mouse sphi 806.2 51.3 1559 21 AAZ47168 Mouse sphi 510.2 32.4 687 22 AAH10443 Lung cance 388.8 23.4 675 22 AAH07214 Human cDNA 319.6 20.3 604 22 AAH0443 Human cDNA 262.8 16.7 2380 22 AAH0441 Human cDNA 262.8 16.7 2422 23 AAS85331 DNA encodi 240 15.3 240 22 AANB4478	Drosophila melanog	ABL03297	23	2020		91.4	37	
1428.4 90.8 1438 22 AAC15936 1168.6 74.3 1205 22 AAC84161 1165 74.1 1173 24 ABL59532 1163.2 73.9 1200 22 AAC161122 ROMAN SPhil 1163.2 73.9 1200 22 AAC161123 ROMAN SPhil 1163.2 73.9 1200 22 AAC16125 ROMAN SPhil 1163.2 73.9 1200 22 AAC16125 ROMAN SPhil 1163.2 73.9 1200 22 AAC16143 ROMAN SPhil 1163.2 73.9 1200 22 AAC16143 ROMAN SPhil 1163.2 73.3 604 24 ABL66446 ROMAN SPHIL 1164.2 74.2 74.2 74.2 74.2 74.2 74.2 74.2 7	Human ORFX polynuc	ABN22070	24	297		105.8	36	
1428.4 90.8 1438 22 AAC15936 1168.6 74.3 1205 22 AAC84161 1165 74.1 1173 24 ABL59552 1163.2 73.9 1200 22 AAC161122 Human sphingo 153.4 54.3 1815 21 AAC17167 853.4 54.3 1815 21 AAC17167 853.2 54.2 1759 22 AAC16425 806.2 51.3 1559 21 AAC17168 806.2 51.3 1559 21 AAC17168 806.2 32.4 675 22 AAC16443 387.6 24.6 675 22 AAC16443 387.6 24.6 675 22 AAC16443 387.6 24.6 675 22 AAC16817 188.6 16.7 2380 22 AAC16817 199.6 16.7 2422 23 AAC18817 199.7 242 24 ABL59533 262.8 16.7 2422 23 AAC18816 240 15.3 240 22 AAC1478 199.7 12.3 296 22 AAC1478 188.2 12.0 2136 22 AAC1477 199.7 12.3 296 22 AAC1477 199.7 12.3 2	Drosophila melanog	ABL02327	23	2830		110.6	35	
1428.4 90.8 1438 22 AACI5936 Human polynuc 1168.5 74.3 1205 22 AACR84161 Human sphingo 1165.5 74.1 1173 24 ABL59532 Human sphingo 1163.2 73.9 1200 22 AAI61122 Human polynuc 853.4 54.2 1759 22 AADH4425 Mouse sphingo 806.2 51.3 1859 21 AAZ47168 Mouse sphingo 806.2 51.3 1559 21 AAZ47168 Mouse sphingo 807.2 24.6 394 24 ABL66446 Lung cancer r 387.6 24.6 394 24 ABL66446 Lung cancer r 388.8 23.4 675 22 AAH07214 Human cDNA c1 319.6 20.3 604 22 AAH04943 Human cDNA c1 262.8 16.7 2380 22 AAS14817 Human cDNA c1 262.8 16.7 2422 <td< td=""><td>an nervous sys</td><td>ABA18278</td><td>22</td><td>11096</td><td></td><td>112.8</td><td>34</td><td>• •</td></td<>	an nervous sys	ABA18278	22	11096		112.8	34	• •
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1428.4 90.8 1438 22 AAC15936 Human polynuc 1168.6 74.3 1205 22 AAC184161 Human sphingo 1165.5 74.1 1173 24 ABL59532 Human sphingo 1163.2 73.9 1200 22 AAC161122 Human polynuc 853.2 54.2 1759 22 AAD14425 Mouse sphingo 865.2 51.3 1559 21 AAZ47168 Mouse sphingo 815.2 24.4 319.5 21 AAZ47168 Mouse sphingo 810.2 32.4 687 22 AAH10443 Human cDNA cl 387.6 24.6 394 24 ABL66446 Human cDNA cl 388.8 23.4 675 22 AAH07214 Human cDNA cl 389.6 28.0 380 22 AAH04943 Human cDNA cl 362.8 16.7 2380 24 ABL59533 Human cDNA cl 262.8 16.7 2482 <	ovarian	ABQ54324	24	1394	•	112.8	32	
1428.4 90.8 1438 22 AACS 436 1168.5 74.1 1173 24 ABL59532 1163.2 73.9 1200 22 AACS 4161 853.4 54.3 1815 21 AACS 4716 855.3 54.2 1759 22 AADS 4425 806.2 51.3 1559 21 AACS 4716 8510.2 32.4 587 22 AADS 446 368.8 23.4 587 22 AADS 446 368.8 23.4 675 22 AADS 446 368.8 23.4 675 22 AADS 481 262.8 16.7 2380 24 ABL5953 262.8 16.7 2380 24 ABL5953 262.8 16.7 2380 24 ABL5953 262.8 15.7 2698 22 AAS 481 246.8 15.7 2698 22 AAS 481 246.8 15.3 296 22 AAS 481 193 12.3 296 22 AAS 487 193 12.3 296 22 AAS 497 181.6 11.5 801 22 AAS 923	kinase	AAD08644	22	1521		116	31	
1428.4 90.8 1438 22 AACS 936 1168.5 74.1 1173 24 ABL59532 1163.2 73.9 1200 22 AACS 1167 853.4 54.2 1759 22 AACS 1167 853.2 54.2 1759 22 AACS 1168 510.2 32.4 58.3 1559 21 AAC 47168 510.2 32.4 58.7 22 AACS 1164 388.6 23.4 675 22 AACS 1164 368.8 23.4 675 22 AACS 1164 319.6 20.3 604 22 AACS 1167 262.8 16.7 2380 22 AACS 1168 262.8 16.7 2380 24 ABL59533 262.8 16.7 2402 23 AACS 1168 263.8 12.3 296 22 AACS 1168 264.0 15.3 296 22 AACS 1172 181.6 11.5 801 22 AACS 1172		AAK92477	22	539	•	132.6	30	
1428.4 90.8 1438 22 AACS 336 1168.4 90.8 1205 22 AACS 4161 1165 74.1 1173 24 ABL59532 1163.2 73.9 1200 22 AACS 4161122 853.4 54.3 1815 21 AACS 4716 853.2 54.2 1759 22 AACS 4716 850.2 51.3 1559 21 AACS 4716 510.2 32.4 587 22 AACS 476 387.6 24.6 394 24 ABL56446 368.8 23.4 675 22 AACS 481 319.6 20.3 264 22 AACS 481 266.2 816.7 2380 22 AACS 481 266.8 16.7 2380 22 AACS 481 262.8 16.7 2380 24 ABL5953 262.8 16.7 2482 23 AACS 481 264.8 15.7 2462 23 AACS 481 264.8 15.7 2468 23 AACS 481 264.8 15.7 2468 23 AACS 481 264.8 15.7 2468 22 AACS 481 265.8 15.7 2468 22 AACS 481 266.8 15.7 2468 22 AACS 487 193 12.3 296 22 AACS 487 193 12.3 296 22 AACS 487 188.2 12.0 2136 22 AACS 487	protein enc	AAH99234	22	801	•	181.6	29	
1428.4 90.8 1438 22 AACH59336 1168.6 74.1 1173 24 ABL59532 1163.2 73.9 1200 22 AACH161 853.4 54.3 1815 21 AACA47167 853.2 54.2 1759 22 AADH1425 806.2 51.3 1559 21 AACA47168 510.2 32.4 587 22 AAH10443 387.6 24.6 394 24 ABL56446 368.8 23.4 675 22 AAH0243 319.6 20.3 604 22 AAH04943 319.6 20.3 604 22 AAH04943 3262.8 16.7 2380 24 ABL5953 262.8 16.7 2380 24 ABL5953 262.8 16.7 2380 24 ABL5953 262.8 16.7 2422 23 AASS14816 240 15.3 240 22 AAS14816 240 15.3 240 22 AAS14816 193 12.3 296 22 AAS14816		AAK94172	22	2136	•	188.2	28	
1428.4 90.8 1438 22 AACH59336 1168.5 74.1 1173 24 ABL59532 1163.2 73.9 1200 22 AACH161127 853.4 54.3 1815 21 AACH7167 853.5 54.2 1759 22 AADH4425 806.2 51.3 1559 21 AACH7168 510.2 32.4 587 22 AADH2446 510.2 32.4 587 22 AAH10443 387.6 24.6 394 24 ABL66446 368.8 23.4 675 22 AAH07214 319.6 20.3 604 22 AAH04943 262.8 16.7 2380 24 ABL59533 262.8 16.7 2380 27 AACH34816 240 15.3 240 22 AACH4816 240 15.3 296 22 AACH4816		AAH83083	22	296	•	193	27	
1428.4 90.8 1438 22 AACS 336 1168.4 90.8 1205 22 AACS 4161 1165 74.1 1173 24 ABL59532 1163.2 73.9 1200 22 AACS 4161122 1163.2 73.9 1200 22 AACS 4161122 1163.2 73.9 1200 22 AACS 4167 853.4 54.3 1185 21 AACS 47167 853.2 54.2 1759 22 AACS 47168 806.2 51.3 1559 21 AACS 47168 510.2 32.4 587 22 AACS 47164 387.6 32.4 675 22 AACS 4716 388.8 23.4 675 22 AACS 4716 368.8 23.4 675 22 AACS 4716 319.6 20.3 264 22 AACS 4716 262.8 16.7 2380 22 AACS 4716 262.8 16.7 2482 23 AACS 4716 262.8 16.7 2482 23 AACS 4716 262.8 16.7 2482 23 AACS 4716 240 15.3 240 22 AACS 4716	Human ovarian PCR-	AAS24477	22	296		193	26	
1428.4 90.8 1438 22 AACH59336 1168.6 74.1 1173 24 ABL59532 1163.2 73.9 1200 22 AACH161 1163.2 73.9 1200 22 AACH16122 1853.4 54.3 1815 21 AACH7167 1853.4 54.2 1759 22 AADH1425 1806.2 51.3 1559 21 AACH1043 1806.2 51.3 1559 21 AACH1043 1807.6 24.6 394 24 ABL66446 1808.8 23.4 587 22 AAH10443 1808.8 23.4 675 22 AAH02943 1809.8 16.7 2380 22 AACH1817 1809.8 16.7 2380 24 ABL59533 1809.8 16.7 2422 23 AACH1817 1809.8 16.7 2422 23 AACH1817	Conserved region D	AAD04478	22	240		24	25	
1428.4 90.8 1438 22 AAC159336 1168.5 74.1 1173 24 ABL59532 1163.2 73.9 1200 22 AAC161122 853.4 54.3 1815 21 AAC147167 855.3 54.2 1759 22 AAD14425 806.2 51.3 1559 21 AAC147168 510.2 32.4 587 22 AAD10443 387.6 24.6 394 24 ABL56446 368.8 23.4 675 22 AAD17214 319.6 20.3 604 22 AAD4943 262.8 16.7 2380 24 ABL5953 262.8 16.7 2380 24 ABL5953 262.8 16.7 2380 23 AAS85331	Mouse cDNA for sph	AAS14816	22	2698		Ġ	24	
1428.4 90.8 1438 22 AAN159336 1168.4 90.8 1205 22 AAR84161 1165 74.1 1173 24 ABL59532 1163.2 73.9 1200 22 AAR161122 853.4 54.3 1815 21 AAR47167 853.2 54.2 1759 22 AAR1425 806.2 51.3 1559 21 AAR47168 510.2 32.4 587 22 AAR10443 387.6 24.6 394 24 ABL56446 368.8 23.4 675 22 AAR107214 319.6 20.3 6044 22 AAR107214 319.6 20.3 604 22 AAR104813 262.8 16.7 2380 22 AAR104813	DNA encoding novel	AAS85331	23	2422	•	2	23	
1428.4 90.8 1438 22 AAC159336 Human 1168.6 74.3 1205 22 AAC84161 Human 1165.7 74.1 1173 24 ABL59532 Human 1163.2 73.9 1200 22 AA161122 Human 853.4 54.3 1815 21 AA247167 Mouse 853.2 54.2 1759 22 AA114425 Mouse 806.2 51.3 1559 21 AA247168 Mouse 510.2 32.4 587 22 AAH10443 Human 387.6 24.6 394 24 ABL66446 Human 319.6 20.3 604 22 AAH07214 Human 319.6 20.3 604 22 AAH04943 Human 319.6 20.3 604 22 AAH04943 Human 319.6 20.3 604 22 AAS14817 Human	Human sphingosine	ABL59533	24	2380	•	3	22	
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1428.4 90.8 1438 22 AAC159336 Human 1168.6 74.3 1205 22 AAC84161 Human 1165 74.1 1173 24 ABL59532 Human 1163.2 73.9 1200 22 AAC161122 Human 1163.2 73.9 1200 22 AAC161122 Mouse 853.4 54.3 1815 21 AAC47167 Mouse 853.2 54.2 1759 22 AAD14425 Mouse 806.2 51.3 1559 21 AAC47168 Mouse 510.2 32.4 587 22 AAD16443 Human 387.6 24.6 394 24 ABL66443 Luman 388.8 23.4 675 22 AAD107214 Human	cDNA clone	AAH04943	22	604	•	9	20	
1428.4 90.8 1438 22 AAI59336 Human 1168.6 74.3 1205 22 AAC84161 Human 1165 74.1 1173 24 ABL59532 Human 1163.2 73.9 1200 22 AAI61122 Human 1853.4 54.3 1815 21 AAZ47167 Mouse 8053.2 54.2 1759 22 AAD14425 Mouse 806.3 51.3 1559 21 AAZ47168 Mouse 510.2 32.4 587 22 AAD10443 510.2 32.4 587 22 AAH10443 Human 387.6 24.6 394 24 ABL66446 Lung	n cDNA clone	AAH07214	22	675	•	œ	19	
1428.4 90.8 1438 22 AAC159336 Human 1168.6 74.1 11205 22 AAC84161 Human 1165 74.1 1173 24 ABL59532 Human 1163.2 73.9 1200 22 AA161122 Human 1853.4 54.3 1815 21 AAC47167 Mouse 853.2 54.2 1759 22 AA1914425 Mouse 806.2 51.3 1559 21 AAC47168 Mouse 510.2 32.4 587 22 AA110443 Human	cancer rela	ABL66446	24	394	•	7	18	
1428.4 90.8 1438 22 AA159336 Human 1168.6 74.3 1205 22 AAC84161 Human 1165 74.1 1173 24 ABL59532 Human 1163.2 73.9 1200 22 AA161122 Human 853.4 54.3 1815 21 AA247167 Mouse 855.2 54.2 1759 22 AAD1425 Mouse 806.2 51.3 1559 21 AA247168 Mouse	cDNA clone	AAH10443	22	587	•	0	17	
1428.4 90.8 1438 22 AAI59336 Human 1168.6 74.3 1205 22 AAC84161 Human 1165 74.1 1173 24 ABL59532 Human 1163.2 73.9 1200 22 AAI61122 Human 853.4 54.3 1815 21 AAZ47167 Mouse 853.2 54.2 1759 22 AAD14425 Mouse	sphingosine	AAZ47168	21	1559	•	٠ ق	16	
1428.4 90.8 1438 22 AAI59336 Human 1168.6 74.3 1205 22 AAC84161 Human 1165 74.1 1173 24 ABL59532 Human 1163.2 73.9 1200 22 AAI61122 Human 853.4 54.3 1815 21 AA247167 Mouse	consensus s	AAD14425	22	1759	•	ω.	15	
1428.4 90.8 1438 22 AA159336 Human 1168.6 74.1 1205 22 AAC84161 Human 1165 74.1 1173 24 ABL59532 Human 1163.2 73.9 1200 22 AA161122 Human	sphingosine	AA247167	21	1815		ω̈́	14	
1428.4 90.8 1438 22 AAI59336 Human 1168.6 74.3 1205 22 AAC84161 Human 1165 74.1 1173 24 ABL59532 Human	polynucleot	AA161122	22	1200	•	ω̈	13	
1428.4 90.8 1438 22 AAI59336 Human 1168.6 74.3 1205 22 AAC84161 Human		ABL59532	24	1173	•	16	12	
1428.4 90.8 1438 22 AAI59336 Human		AAC84161	22	1205	•	1168.6	11	
	Human polynucleoti	AAI59336	22	1438	•	1428.4	10	

ALIGNMENTS

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RESULT 1
AAA75676
neurological disorder; Parkinson's disease; demyelinating disease; meningitis; developmental disorder; neuromuscular disorder; cancer; myasthenia gravis; cell proliferative disorder; actinic keratosis; arteriosclerosis; atherosclerosis; leukaemia; melanoma; bronchitis; autoimmune disorder; inflammatory disorder; Addison's disease; acquired immunodeficiency disease; allergy; diabetes mellitus; rheumatoid arthritis; microbial infection; trauma; ss.
                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                      Human; intracellular phosphorylation regulator; HRIP; stroke; myeloma;
                                                                                                                                                                                                                                                                                                                                                    DNA encoding a human regulator of intracellular phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                   AAA75676;
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA75676 standard; DNA; 1573
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                   Location/Qualifiers
                                                                                                    /product= "regulator of intracellular phosphorylation"
                                                                                                                    /*tag=
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AAA50508

Human

Human

17-MAR-2000; 2000WO-US07277

21-SEP-2000. WO200055332-A2

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The present sequence encodes a human regulator of intracellular phosphorylation (HRIP). HRIP is useful for screening agonists and antagonists of HRIP pollypeptide. HRIP and its agonist or antagonist and cancer as the set of the sequence of the sequence of the sequence of the decreased with decreased or increased expression of functional HRIP. Diseases treated cor diagnosed include neurological disorders such as stroke, parkinson's disease, demyelinating diseases, bacterial and viral meningitis and other developmental disorders, myasthenia gravis, cell proliferative disorders such as actinic keratosis, arteriosolerosis, atherosolerosis and cancer including leukaemia, melanoma, myeloma and cancer of the adrenal gland, bladder, bone, bone marrow, liver, lung, muscle, ovary, autolmunoc/ infinammatory disorder such as Addison's disease, acquired inmunodeficiency diseases, allargies, bronchitis, diabetes mellitus, or rheumatold arthritis, microbial infection and trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 1573; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1999;
20-MAY-1999;
09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human intracellular phosphorylation regulator polypeptides and polynucleotides for diagnosis, prevention and treatment of neurological, cell proliferative and autoimmune/inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 89; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-602121/57
P-PSDB; AAB18659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1573 BP; 274 A; 480 C; 514 G; 305 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE PHARM INC.
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                    GAGACGCCATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGCGCTCTGGCAACGCGCTGGCA 480
                                                                                                                ATGTCTGGAGACGGGCTGATGCACGAGGTCGTGAACGGGCTCATGGAGCGGCCTGACTGG
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Au-Young J;
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99US-0135049.
99US-0143188.
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100.0%; Pred. No. 0;
Live 0; Mismatches
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  1561 AAAAAAAAAAAA 1573
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781 GTGGGTTCCAAGACACCTGCCTCCCCCGTTGTGGTCCAAGCAGGGCCCGGTAGATGCACAC
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                                                                         TIGTICTGAGACCCCCACCCCACGAACCAAATCCAAATAAAGTGACATTCCCAGCCTGAA 1560
                                                                                                                                     GAAGTCCTGGGTCAGGAGCCCAGCTGGCTGGGCCCAGCTGCCTATGTAAGGCCTTCCTAGT
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                                               TTGTTCTGAGACCCCCACCCACGAACCAAATCCAAATAAAGTGACATTCCCAGCCTGAA
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                                                                                                                                cc of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end cc sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CC cDNAs easily without any specialised methods. AAH33166 to AAH33628 and CC AAB5383 represent human canid sequences; and AAH33629 to AAH33632 represent numan amino acid sequences; and AAH3629 to AAH33632 represent oligonucleotides, all of which are used in the exemplification
Query Match
Best Local Similarity
Matches 1558; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                  AAB95893 represent human amino represent oligonocleotides, all of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                         to the complementary strand of a polynucleotide which comprises one the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combinate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprises:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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27-AUG-1999;
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Sugiyama T, Wakama
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; 2000JP-0183767.
; 2000JP-0241899.
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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99JP-0300253
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A, Nagai
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29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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                         Claim 8; SEQ ID 15393; 2537pp + CD ROM; English
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The present invention describes primer sets for synthesising
                                                                                                          WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy;
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                                                                                                                                             Isogai T,
                                                                                                                              sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                          2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                              99JP-0248036
99JP-0300253
                                                                                                                                Hayashi K,
A, Nagai
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                                                                                                                                             Yamamoto
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γQ В 8 밁 Ş В δÃ 밁 Ş рь á g 20 В

cc full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligo-dto comprises complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a polynucleotide which comprises a 3'-end sequence, where the coligonucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises a 3'-end sequence, where the coligonucleotide comprises as 1 nucleotides and the combination of the 5'-end sequence'3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, complementary to a particularly full-length cDNAs. The primers are useful for synthesising polynucleotides, continuated the specification and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are useful for synthesis of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are primers allow obtaining

Sequence 1772 BP; 285 A; 566 C; 585 G; 336 T; 0 other;

Score 1539.4; DB 22; Length 1772; Pred. No. 0; 0; Mismatches 1; Indels 1; 1; Gaps

1;

120 GGTCGAGGTTATGGATCCAGCGGGCGGGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGCGT 179 220 GCCCCACAGCCGGCCCTGCGACGCCCGCCTGGGCAGCCGATAAGGAGCTGAAGGCAGC 279 280 AGCCGCCGCCACGGGCAGCGCCCCCACAGCGCCAGGGACCCCCTGGCAGCGGGAGCCGCG 1 GCCCCACAGCCGGCCCTGCGACGCCCGGCCTGGGCAGCACCGATAAGGAGCTGAAGGCAGG 60 GGAGACCGCCATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCGCTGGC GAACCACGCGCGGGAGCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGT GGAGACCGCCATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAACGCCCTGGC GAACCACGCGCGGGAGCTGGTGCGGTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGT CGTGCAGCCCCTTTTTGGCTGAAGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCG GGTCGAGGTTATGGATCCAGCGGGCGGCCCCCGGGGCCGTGCTCCCGCGGCCCTGCCGCGT CGTGCAGCCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGCG GCTGGTGCTGCAACCCGCGCGGCGGCAAGGGCCAAGGCCTTGCAGCTCTTCCGGAGTCA GCTGGTGCTGCTGAACCCGCGCGGCGGCAAGGGCCAAGGCCCTTGCAGCTCTTCCGGAGTCA 239 AGCCGCCGCCACGGGCACCG-CCCCACAGCGCCACGGGACCCCTGGCAGCGGGGAGCCGCG 119 699 479 579 359 399 339

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Human; sphingosine kinase type 1; sk1; chromosome 17q25.2; sphingosine-1-phosphate; S1P; drug screening; therapy; haemos thrombosis; allergic reaction; proliferative disease; cancer;
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                                           Human sphingosine kinase type 1 (hsk1) cDNA
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Matches 1548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atherosclerosis; coronary artery disease; dyslipidaemia; diabet autoimmune disease; inflammatory disease; multiple sclerosis; Thelper-1 related disease; chronic obstructive pulmonary diseasthma; myocardial infarction; neurodegenerative disorder; wound healing; embryogenesis; anticoagulant; cerebroprotective;
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P-PSDB; AAE07882.
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22-MAR-2000; 2000US-0191261
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Claim 8; Page 89-90; 107pp; English

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                                                  GAGACTCCTCTGGAGAAGGGTGAGAAGGTGGAGGCTATGCTTTGGGGGGGACAGGCCAGAA
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01-MAR-1999 entry)

secreted gene 80 clone HNFAE54.

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukami developmental abnormality; foetal deficiency; blood; allergy; renal; ds immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymu osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; regulation; ia;

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18-DEC-1997
06-JUN-1997
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05-SEP-1997;
05-SEP-1997;
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P-PSDB; AAW88613.
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                              245 AGCCCCTTTTGGCTGAAGCTGAAATCTCCTTCACCCTGATGCTCACTGAGCCGCGCAGAACC
305 ACGCGCGGGAGCTGCTGCGGTCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGGTCATGT
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B GCCGNCACGGCAGCGCCCATAGCGCCAGGGACCCCCTGGCAGCGGGAGCCGCGGGTCG 67
                                                                                                TGCTGCTGAACCCGCGCGGCGCAAGGGCCAAGGCCCTTGCAGCTCTTCCGGAGTCACGTGC
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97US-0057760.

97US-0057763.

97US-0057769.

97US-0057774.

97US-00577777.
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New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                      Brewer LA, Carter KC, Dillon PJ, Ebner R, Endrener Fran P, Feng P, Ferrie AM, Fischer CL, Florence C Florence K, Greene JM, Hu J, Kyaw H, Lafleur DW; Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruber Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
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ence C;
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CC encoding human secreted proteins (AAW88453) to AAW88756). The secreted concoding human secreted proteins (AAW88754) to AAW88756). The secreted concoding human sequences are deposited with the ATCC under deposit numbers can gene sequences are deposited with the ATCC under deposit numbers concoding the nucleic acid sequences are sequences are deposited with the ATCC under deposit numbers colored to the comprising recombinant vectors containing the nucleic acid sequences are used for the recombinant production of the secreted consequences are useful for preventing treating or ameliorating medical conditions e.g. to proteins. The polynucleotide and amino acid sequences are useful for are combinant vectors containing the nucleic acid sequences are useful for for preventing treating or ameliorating medical conditions e.g. to protein or gene therapy. Pathological conditions can be also comprised by determining the amount of the new polynucleotides. It is a sample compared to the production of the polynucleotides are described for each of the polynucleotides are developing conditions in the new polynucleotides. Specific uses are described for each of the polynucleotides are also conditions for the diagnosis or treatment of cancer, neurodegenerative condisorders, tumours, leukemias, diseases of the immune system, autoimmune conditions to the present separatic and renal diseases. Jumphomas, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schloophrenia, created sexually prostate diseases, obesity, disorders, diseases of testes.

CC unds or thymus, disestive/endocrine disorders, diseases of testes.

CC unds or thymus, disease, obesity, disorders involving osteoclasts conditions are also useful for identifying their binding partners.

CC the present sequence represents a gene encoding a human secreted protein conditions and clone identification).

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                        CCCTTCCTCCTTCCCTAGGGCTGCAGGGCCTGTCCACAGCTCCTGTGGGGGTGGAGGAGA
                                                                                    CCGCCAGAAGAGCCCCTATGACCCCCTGGGCCGCGCTGTGCCTTAGTGTCTACTTGCAGGA
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ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secrete proteins (I) and polynucleotide (II) sequences. (I) and (II) have variactivities based on the tissues and cells the genes are expressed in. Example of these activities include: immunomodulatory; antisclerotic; dermatological; immunosuppressive; antiinflammatory; immunostimulant; anti-HIV, cytostatic; cardiant; anti-anglogenic; ophthalmological; neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;

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Tence C,
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29-MAR-2000;
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Soppet DR, Young PE, Shi Y, Florence KA, I
C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie,
Endress GA, Dillon PJ, Carter KC, Brewer LA,
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2000US-193170P.
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Ferrie AM, Fan
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Best Local Similarity
Matches 1432; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia an epilepsy; and (f) infectious diseases such as viral, bacterial, fung and parasitic infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamalytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's allergies autoimmune thyroiditis, diabetes mellitus, crohn's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                  ATGCTGGCTATGAGCAGGTCACCAATGAAGACCTCCTGACCAACTGCACGCTATTGCTGT
                                                                                                                  AGCCCCTGTGTAGCCCTCCCAGCAGGCTCTGGCAACGCGCTGGCAGCTTCCTTGAACCATT
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                                                                                                          GGGTGAGAAGGTGGAGGCTATGCTTTGGGGGGGACAGGCCAGAATGAAGTCCTGGGTCAGG
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                                         AGCCCAGCTGGCCTGGCCCAGCTGCCTATGTAAGGCCTTCTAGTTTGTTCTGAGACCCCC
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                       B
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CC The polynucleotide was isolated from an HeLa cDNA library by CP CR amplification. The invention provices polynucleotides (see AAA96057-59) for the human cC sphingosine kinase (SK) bomologues SKA, SKB and SKC. The cC polynucleotides may be used as hybridization probes, in the CC primers for chromosome and gene mapping, in the CC construction of PCR primers for chromosome and gene mapping, in CC the recombinant production of SKA, SKB and SKC, and in the CC enstruction of antisense DNA or RNA. They can be used to detect inflammation or disease associated with abnormal levels of SK contains and carrier or affected individuals. Host cells expressing CC inflammation or affected individuals. Host cells expressing CC inflores, ligands or their analogues can be used as bioactive agents to treat inflammation or disease including viral, bacterial CC associated with trauma, hereditary disease, mechanical injury can other conditions with activate the genes of kidney, lung, heart, lymphoid or tissues of the nervous system.
                                                                                                                                                                      Matches 1436; Conservative
                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human sphingosine kinase A, B and C polynucleotides and polypeptides useful in e.g. chromosome and gene mapping, and detecting inflammation or disease associated with abnormal levels of sphingosine kinase expression -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sphingosine kinase A; SKA; human; drug screening; infection; antiinflammatory; antiallergic; anticancer; inflammation; allergy; cancer; therapy; diagnosis; ds.
                                                                                                                                                                                                                                             Sequence 1447 BP; 256 A; 427 C; 465 G; 299 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-572185/53.
P-PSDB; AAY06057.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kinase expression
                                                            184 CTGCTGCTGAACCCGCGCGGCGAGGGCAAGGCCCTTGCAGCTCTTCCGGAGTCACGTG 243
                                                                                                                                 124 GAGGTTATGGATCCAGCGGGCGGCCCCCGGGGCCCTGCCGCGGCCCTGCCGG
                       61 GTGCTGCTGAACCCGCGGGGCAAGGGCAAGGGCTTTGCAGCTCTTCCGGAGTCACGTG 120
                                                                                                                                                                                           Local Similarity
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                                                                                            GAGGTTATGGATCCAGCGGCCGCCCCCGGGGCGTGCTCCCGCGGCCCTGCCGCGTGCTG 60
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                                                                                                                                                                                       90.98;
                                                                                                                                                                      0; Mismatches 11; Indels
                                                                                                                                                                                     Score 1429.4; DB 2
Pred. No. 6.3e-310;
                                                                                                                                                                                                        DB 21; Length 1447;
                                                                                                                                                                      0; Gaps
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1324 CCCTTCCTTCCCTAGGGCTGCAGGGCCTGTCCACAGCTCCTGTGGGGGGTGGAGGAGA 1383
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TCTACTTGCAGGA 13 	64 CCGCCAGAAGAGCCCTTATGACCCCTGGGCCGCCCTGTGCCCTTAGTG	Qy 12 Db 11		
CCAGCAGATGCCA 126	04 TTCTGGATGGTCAGCGGTTGGGTGGAGCCCCCGCCCAGCTGGAAGCC 	Oy 12 Db 10		
GCACCCAAACTAC 120 	144 GCAGTGGATGGGGAATTGATGGTTAGCGAGGCCGTGCAGGGCAGGTG	Qy 11 Db 10		
GAAAGGTGTGTTT 114)84 TIGGTATATGTGCCCGTGGTCGCCTTCCGCTTGGAGCCCAAGGATGGG 	Qy 10 Db 9		
STATGAATGCCCCTAC 108 	24 CTGCTGCGCCTCTTCCTGGCCATGGAGAAGGCAGGCATATGGA 	Qy 10 Db 9		
STCTCGTGCCATG 102 STCTCGTGCCATG 900	64 CGCTGTGCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGG	Оу 9 Др. 8		
TGCACCCATGGGC 963	04 CTAGTCCTGCCACTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGC	Oy 9 Db 7		
CGAGGACTTTGTG 903	44 GTGCCACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGA	Qy 8 Db 7		
AGATGCACACCTT 843	84 GGTTCCAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGCCCGGT	ОУ 7 ръ 6		
TGTAGGAAGAGTG 783 	24 CGTCTGGCAGCCCTGCGCACCTACCGCGGCGACTGGCCTACCTCCC	Qy 7		0
GGCACCTTCCTG 723 HIIIIIIIIIII GGCACCTTCCTG 600	564 CTAGAGAGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCTTCACTCTGG 	Qy 6	-	
RGCTGATGTGGAC 663 RGCTGATGTGGAC 540	104 reasgaetgeaceterfetetgtaetelaacetgacetgaactteatt 	Qу 6 рь 4	н' а	
TCTGCACACGGCT 603 TCTGCACACGGCT 480	44 ACGCTATTGCTGTGCCGCCGGCTGCTCACCCATGAACCTGCTGTC	Qу 5 Db 4		
CTGACCAACTGC 543	84 TCCTTGAACCATTATGCTGGCTATGAGCAGGTCACCAATGAAGACCTC 	Qy 4 Db 3		
GCGCTGGCAGCT 483	24 ACCGCCATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTGGCAAC	Qy 4 Db 3		
CCTGACTGGGAG 423	364 TCTGGAGACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGG	Qy 3		
SCTCTGGTGGTCATG 363 	04 CACGCGCGGAGCTGCTGCTGCGAGGAGCTGGGCCCCTGGGACC	Qy 3		
CACTGAGCGGCGGAAC 303	4 CAGCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCT 21 CAGCCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCT 21 CAGCCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCT	Db 1		
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
14-SEP-2000;
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    The invention relates to human nucleic acids (AAI57799-AAI61369) the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are in gene therapy. A composition containing a polypeptide or polynof the invention may be used to treat diseases of the peripheral
                                                                                                                                      Claim
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leukaemia; ss
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DB; AAM40180.
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2000US-0552317.
2000US-0598042.
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2000US-0653136.
2000US-0633336.
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Matches 1432
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Pred. No. 1.1
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                                  13-MAY-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                   Human sphingosine kinase encoding cDNA.
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(JOHJ ) JOHNSON & JOHNSON RES PTY LTD
                                                                                   12-MAY-2000;
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                                  99AU-0000339.
99AU-0001504.
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33..1187
/*tag= a
                                                                                                                                                                                   /product= "sphingosine kinase"
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This cDNA encodes a human sphingosine kinase (SK) protein. The human SK protein, encoding nucleic acids and modulators are useful for modulating expression, functional activity or cellular functional activity of sphingosine kinase in a subject and also for treating a mammal by modulating the activity of SK. Diseases treated by regulating SK cellular activity include rheumatoid arthritis, astima, atheroscierosis, inflammation, meningitis, multiple scierosis and septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel sphingosine kinase protein and nucleic acid molecules for diagnosis, prophylaxis and treatment of rheumatoid arthritis, asthma, atherosclerosis, inflammation, meningitis, multiple sclerosis and septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1205 BP; 196 A; 357 C; 400 G; 252 T; 0 other; .
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        TRCTYCACTGAGGGGGGGAACCACCGCGGGAGGAGCTGGGTCCGGTCGGAGGAGGAGCTGGGCCCCT
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        214
        TRCTYCACTGAGCGGCGGAACCACCGCGGGAGGAGCTGGTCCGGAGGAGGAGCTGGGCCGCT
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        187
        TGCTCACTGAGCGGGAACCACGCGGGGAGCGAGCTGGGCCGGTCGGAGGAGCTGGGCCGCT
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                                                                                                                                                                               524 AAGACCTCCTGACCAACTGCACGCTATTGCTGTGCCGCCGGCTGCTGTCACCCATGAACC
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                                                TRACTICTIGGCACCTTCCTGCGTCTGGCAGCCCTGCGCACCTACCGGCCCGACTGGCCT 763
TRACTICTIGGCACTTTCCTGCGTCTGGCAGCCTTGCGCACTTACCGCGGCCGACTGGCTT 666
                                                                                                                                                                                                                TGCTGTCTCTGCACACGGCTTCGGGGCTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGG 643
                                                                                                                                                                                                                                                                                                                                                                                                      TGGAGCGGCCTGACTGGGAGACCGCCATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCT 463
                                                                                                                 GCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGGAGATGCGCT
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Similarity 99.2%;
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  characteristics, comprising measuring of at least two genes associated with
                                                                 Identifying tumor characteristics in a tissue sample taken patient, involves determining the copy number or expression genes associated with lipid metabolism, synthesis or action
                                                                                                                                                                              28-SEP-2000;
                                                                                                                                                                                                    27-SEP-2001;
                                                                                                                                                                                                                         04-APR-2002
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                                                                                                                                                                                                                                                                     Homo
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                                            Example 1; Page 90; 113pp; English.
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present invention describes a method for identifying tumour racteristics, comprising measuring a copy number or expression at least two genes associated with lipid metabolism, synthesis.
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Best Local Similarity
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                                                                                                                             GCTGATGTGGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGAGATGCGCCTTCACTCTG
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 GATGCACACCTTGTGCCACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGAC
                                                        GTAGGAAGAGTGGGTTCCAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTA
                                                                                                                GGCACTTTCCTGCGTCTGGCAGCCTTGCGCACTTACCGCGGCCGACTGGCTTACCTCCCT
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D; Mismatches
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GAGGACTTTGTGCTAGTCCTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTTTGCT

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ARESULT 13
AA161122
XX AA161122
XX AA161
AC AA16
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25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0623450.

14-SEP-2000; 2000US-0652191.

19-OCT-2000; 2000US-0652191.

29-NOV-2000; 2000US-0727344.
Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; nootxopic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; cNS; Alzheimer's; Parkinson's disease; Huntington's disease; hacmostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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DB; AAM41966.
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Zhou P,
                                                                                                                Asundi V, Chen R, Ma Y, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RT;
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               for treating
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                  disorders
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification.
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TGCTGCGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCCTACT
                                                                                                                                                                                                                                                                                                                                                                                                     GTTCCAAGACACCTGCCTCCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACGTTG
                                                                                                                                                                                                       TAGTCCTGGCACTGCTGCACTCGCCACCTGGCCAGTGAGATGTTTGCTGCACCCATGGGCC
                                                                                                                                                                                                                                                                                                   TGCCACTGGAGGAGCCAGTGCCCTCTCACTGGACAGTGGTGCCCGACGAGGAGTTTGTGC
                                              TGCTGCGCCTCTTCCTGGCCATGGAGAAGGGCAGGCATATGGAGTATGAATGCCCCCTACT 108
                                                                                                                          GTCTGGCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACCTCCCTGTAGGAAGAGTGG
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99.2%; Pred. No. 1.96
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P-PSDB;
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This sequence represents the coding region for the mouse sphingosine kinase la. The sequence was isolated by searching a dbEST (expressed
                                       New sphingosine kinase, proliferation, e.g. cand
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11-AUG-1998;
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                        Example 1; Page 113-114; 116pp; English.
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98US-0096049
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CTTCCTGCGTCTGGCAGCCCTGCGCACCTACCGCCGACTGGCCTACCTCCCTGTAGG
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second messenger, and confers serum-independent growth; increases proliferation, and suppresses serum-deprivation or ceramide-induced apoptosis. The sphingosine kinase nucleic acid is used: (a) to increase sphingosine kinase content of cells, specifically for reducing cell death and/or increasing cell proliferation; and (b) to produce transfected cells that are used to screen for agents that inhibit or promote sphingosine kinase activity. Agents that reduce sphingosine kinase activity. Agents that reduce sphingosine kinase activity or expression are used: (i) to reduce cell proliferation, specifically for treating cancer, and (ii) to treat diseases associated with abnormal cell migration or motility, particularly cancer, restenosis or diabetic neuropathy (but also atherosclerosis, stroke and Alzheimer's disease), whereas agents that stimulate sphingosine kinase can be used to treat conditions associated with reduced cell proliferation, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence tag database) using amino acid sequence results from sequenced tryptic digests of the rat sphingosine kinase. Expression of sphingosine tryptic digests of the rat sphingosine kinase. Expression of sphingosine tryptic digests of the rat sphingosine of sphingosine-1-phosphate, a known kinase in cells results in formation of sphingosine-1-phosphate, a known
developmental
retardation.
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1815 BP; 382 A; 511 C; 533 G; 389 T; 0 other;

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Local Similarity
es 1171; Conserv
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Mouse; sphingosine kinase; SphK; restenosis; ischaemia; gene therapy; antisense therapy; cancer; sphingolipid; signalling molecule; apoptosis; cytostatic; tumour necrosis factor-alpha; TNF; atherosclerosis; lymphoma
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                                                           Mouse consensus sphingosine kinase (SphK) cDNA.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to sphingosine kinase (SphK) polypeptides and nucleic acids encoding them. SphK is useful for treating a SphK-associated disorder especially cancers such as leukaemia, lymphoma, ovarian, breast, lung, colon, testicular, stomach and skin, atheroscierosis, restenosis or ischaemia and cell proliferative disease or disorder associated with vascular diseases. SphK gene is used in gene therapy and antisense-therapy. Sphingollpids serving as signalling molecules, have recently emerged as regulators of cell growth, diverse cell phenotypes and cell growth, diverse cell phenotypes and cell death. Activation of SphK by tumour necrosis factor (TNF)-alpha inhibits apoptosis in human endothelial cells. The present sequence is consensus mouse sphingosine tinace (Schk) (TNR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1759 BP; 357 A; 495 C; 523 G; 384 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase (SphK) cDNA.
                                                              436 GTGTGCAGCCCTTCCTGGAGGGGGGGGGAGATAACCTTTAAACTGATACTCACCGAACGGA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 92; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated Sphingosine kinase polypeptide usoful for treating a SphK-associated disorder especially cancer, restenosis or ischemia in a
299 GGAACCACGCGCGGGAGCTGCTGCTGCGGAGGAGCTGGGCCGCTGGGACGCTCTGGTGG
                                                                                                                                                    376
                                                                                                                                                                                            179
                                                                                                                                                                                                                                    316
                                                                                                                                                                                                                                                                            119
                                                                                                                                                                                                                                                                                                                   256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CURA-) CURAGEN CORP. (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-FEB-2000;
22-MAR-2000;
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                                                                                                                                           TGCTGGTGCTGAACCCGCGCGCGCGCAAGGGCAAGGCCTTGCAGCTCTTCCAGAGTC
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                                                                                                        ACGTGCAGCCCCTTTTGGCTGAGGCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGC 298
                                                                                                                                                                                                                               GGGACCTGGCTATGGAACCAGTAGAATGCCCTCGAGGACTGCTCCCACGGCCATGCAGAG
                                                                                                                                                                                                                                                GGGTCGAGGTTATGGATCCAGCGGGGGGGCGCCCCCGGGGGCGTGCCGGGGCCCTGCCGGG 178
                                                                                                                                                                                                                                                                                                              CCGCCGTTACCTCTAGCAGCGCCGGGGGCACCGGTGGCCCCTTGTCAGCGGGAGCCCC
                                                                                                                                                                                                                                                                                                                                                    CCGCCGCCACGGGCAGCGCCCC----ACAGCGCCAGGGACCCCCTGGCAGCGGGAGCCGC 118
                                                                                                                                                                                                                                                                                                                                                                                           CCCACGGCCAGTCGCCAGACACCCTCCTGGGCAACACCGATAAGAAGCTGAACGCAGGAG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-514770/56.
DB; AAE07883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 73.9
58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0182360
2000US-0191261
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/product* "Mouse sphingosine kinase (SphK) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 327..1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.2%; Score 853.2; DB 22; Length 1759; 73.9%; Pred. No. 3.9e-181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                           358
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513 GACCCTCCCCGCACCCACCTCCTGGTATGGGAGGTTATTTC 376 GGAGGACTCCTCTGGAGAAGGGTGAAGGTGAGGCTAT 1
CAGAAGACCCTTATGACCCCTGGGCCGCGC
1199 ACTACTTCTGGATGGTCAGCGGTTGGGTGGAGCCCCGCCCAGCTGGAAG
1139 TGTTTGCAGTGGATGGGGAATTGATGGTTAGCGAGGCCCTGCAGGGCC
1079 CCTACTTGGTATATGTGCCCCGTGGTCGCCTTCCGCCTTGGAGCCCAAGGATG
1019 CCATGCTGCTGCGCCTCTTCCTGGCCATGGAGAAGGGCAAGCATATGG
959 TGGGCCGCTGTGCAGCTGGCGTCATGCATCTGTTCTACGTGCGGGCGG
899 TTGTGCTAGTCCTGGCACTGCTGCACTCGCACCTGGGCAGTGAGATGTT
839 ACCITGIGCACIGGAGGAGCCAGIGCCCICICACIGGACAGIGGIGCO
779 GAGTGGGTTCCAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCC
719 TCCTGCGTCTGGCAGCCCTGCGCACCTACCGCGGCCGACTGGCCTACC
659 TGGACCTAGAGAGTGAGAAGTATCGGCGTCTGGGGGGAGATGCGCTTCAC
599 CGGCTTCGGGGCTGCGCCTCTTCTCTGTGCTCAGCCTGGCCTGGGGCTTC
539 ACTGCACGCTATTGCTGTGCCGCCGGCTGCTGTCACCCATGAACCTGCT
479 CAGCTTCCTTGAACCATTATGCTGGCTATGAGCAGGTCACCAATGAAG
419 GGGAGACCGCCATCCAGAAGCCCCTGTGTAGCCTCCCAGCAGGCTCTG
359 TCATGTCTGGAGACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGG
496 AGAACCATGCCAGGGAGCTGGTGTGTGCAGAGGAGTTGGGTCACTGGG

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Search completed: May 17, 2003, 11:14:20 Job time : 412 secs



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Title:
Perfect score:
Sequence:
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 Database :
                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                     US-09-937-060A-5
2016
1 MDPAGGPRGVLPRPCRVLVL.....CVEPPPSWKPQQMPPPEEPL 384
                                                                                                                                                                                                                                                                                                                                         112892 seqs, 41476328 residues
SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                         112892
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

esult No. 1 2 3	0.91.5			DB 1	ID SPH1_HUMAN SPH2_HUMAN SPH2_HUMAN EMRU_BACSU	cr ya ia ia
08750	99.5 93.5 93.5	0444 0000	433 1065 791 712		YUJA_SYNYJ KDGI_HUMAN KDGI_DHOME DNLJ_RHOMR DNLJ_RHOMR	O59452 synechocyst O75912 homo sapien Q01583 drosophila P49421 rhodothermu C10133 Geenerhabdi
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17 18	86.5 86	4 4 	2470 390		NTC2_MOUSE ARP2_SCHPO	035516 mus musculu 09uuj1 schizosacch
19 20	85.5	4.3	448 662		5H7_MOUSE LOX2_PIG	
21 22	യയ	4.2	608 827	بر ب	HFAC_CAUCR KDGL_CAEEL	caul caen
223 25	84.5 84.5	4.2 4.2	335 369 471	ب بن ب	G3P2_METAC XYLM_PSEPU HH_DROME	or or a
26 27 28	ω. a	4.2	492 586	<u> </u>	GVD2_HALN2 TU12_SCHPO	, w w
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3 3 2	82 82	4.1 4.1	873 942	- -	PODK_CLOSY KDGT_HUMAN	2298 5282

45	44	43	42	41	40	39	38	37	36	ω 5	34
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EF3_SCHPO	PEX6_RAT	DHGA_ACICA	LYSR_ECOLI	VG65_HSVI1	CTPG_MYCTU	CMCH_STRCL	BIOA_SERMA	CX1A_PARDE	RURE_ACICA	G3P_PYRAB	DYHB_CHLRE
094489	P54777	P05465	P03030	Q00106	010866	085728	P36568	P08305	P42454	Q9v1p1	039565
schizosacc	rattus nor	acinetobac	escherich	ictalurid	mycobacte	streptomyce	serratia n	paracoccus	acinetobac	pyrococcus	chlamydomo:

ALIGNMENTS

RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RC TISSUE-Ovary, and Mammary gland; RA Isogal T., Oca T., Hayashi K., Sugi: RA Nishikawa T., Nagai K., Sugano S.,; RA Wagatsuma M., Hosoiri T., Kaku Y., RA Takahashi M., Chiba Y., Ishida S., RA Watanabe S., Kimura K., Murakami K. RA Yamamoto J., Wakamatsu A., Nakamura RA Ninomiya K., Iwayanagi T.; RT "NEDO human cDNA sequencing project Submitted (AUG-2000) to the EMBL/Ge CC -!- FUNCTION: Catalyzes the phospho CC sphingosine 1-phosphate (SPP), CC and extracellular functions. Al: and to a lesser extent sphingan CC D,L-threo-dihydrosphingosine, N		· ·	SPH1_HUMAN STAND ID SPH1_HUMAN STAND AC OSNYA1; OSNYL13; OSHD DT 15-JUN-2002 (Rel. 41 DT 15-JUN-2002 (Rel. 41 DT 15-JUN-2002 (Rel. 41 DT 15-JUN-2002 (Rel. 41 DT Sphingosine kinase 1
E FROM N.A. CVARY, and Mammary gland; OVARY, and Mammary gland; T. Ota T., Hayashi K., Sugaiyama T., Otsuki T., Suzuki Y., Ma T., Nagai K., Sugaino S., Shiratori A., Sudo H., Ma T., Nagai K., Sugaino S., Shiratori A., Kondo H., Sugawara M., Ma M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., e S., Kimura K., Murakami K., Tshii S., Kawai Y., Saito K., o J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., a K., Iwayanagi T.; ed (AUG-2000) to the EMBL/GenBank/DDBJ databases. CTION: Catalyzes the phosphorylation of sphingosine to form ingosine 1-phosphate (SPP), a lipid mediator with both intra- extracellular functions. Also acts on D-erythro-sphingosine to a lesser extent sphinganine, but not other lipids, such a -threo-dihydrosphingosine, N.N-dimethylsphingosine,	Nava V.E., Lacana E., Poulton S., Liu H., Sugiura M., Kono K., Milstien S., Kohama T., Spiegel S.; "Functional characterization of human sphingosine kinase-1."; FEBS Lett. 473:81-84(2000). [3] [3] [SI] [SI] [SI] [MEDLINE=20407120; PubMed=10947957; Pitson S.M., D'Andrea R.J., Vandeleur E., Moretti P.A.B., Xia P., Pitson S.M., D'Andrea R.J., Vandeleur E., Moretti P.A.B., Xia P., "Human sphingosine kinase: purification, molecular cloning and characterization of the native and recombinant enzymes."; Biochem. J. 350:429-441(2000). [4] [5] [8] [8] [9] [9] [9] [1] [9] [1] [9] [9] [9] [9] [9] [9] [9] [9] [9] [9	hordata; Craniata; Vertel hordata; Craniata; Vertel rimates; Catarrhini; Hom. Dias E., Gosink M., Allanase: molecular cloning, tissue distribution.";	STANDARD; PRT; 384 AA. L3; O9HD92; Q9NY70; (Rel. 41, Created) (Rel. 41, Last sequence update) (Rel. 41, Last annotation update) kinase 1 (EC 2.7.1.) (SK 1) (SPK 1).

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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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38
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EMBLE, AF238083; AAF73423.1; -
EMBL: AF200328; AAG01980.1; -
EMBL: AK023393; BAB14558.1; -
EMBL: AK023393; BAB14028.1; -
EMBL: AK023402; BAB14028.1; -
EMBL: AK02402; BAB14028.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew;
                                                361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP. SUBUNIT: Binds to calmodulin.
SUBUNIT: Binds to calmodulin.
TISSUE SPECIFICITY: Widely expressed with highest levels in adult liver, kidney, heart and skeletal muscle.
SIMILARITY: BELONGS TO THE SPHINGOSINE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diacylglycerol, ceramide, or phosphatidylinositol.
CATALYTIC ACTIVITY: Sphingosine + ATP = sphingosine 1 phosphate
                                                                                                                                                                                                                                                                                                                                                                                                   NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDPAGGPRGVLPRPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHA 60
MVSGCVEPPPSWKPQOMPPPEEPL 384
                                          MVSGCVEPPPSWKPQQMPPPEEPL 384
                                                                                          RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFW
                                                                                                                                     RLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFW 360
                                                                                                                                                                                                          LEEPVPSHWTVVPDEDFVLVLALLHSHLGSENFAAPMGRCAAGVMHLFYVRAGVSRAMLL 300
                                                                                                                                                                                                                                                                                                     SEKYRRLGEMRETLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP 240
                                                                                                                                                                                                                                                                                                                                                                        NHYAGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLAWGFIADVDLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RELYRSEELGRWDALYVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL 120
                                                                                                                                                                                  LEEPVPSHWTVVPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLL
                                                                                                                                                                                                                                                                             SEKYRRLGEMRFTLGTFLRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00781; DAGKc; 2.
; PD005043; DAG_kin_cat; 1.
SM00046; DAGKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:11240; SPHK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42517 MW;
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6 MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 2016; DB 1; 100.0%; Pred. No. 3.4e-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LERPC - ARL (IN REF. 4).

NA -> KP (IN REF. 2).

V -> M (IN REF. 2).

V -> I (IN REF. 2).

L -> F (IN REF. 2).

V -> G (IN REF. 3).

V -> M (IN REF. 3).

V -> M (IN REF. 3).
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MBL outstation -
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SPH2_MOUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thompson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                     IISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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RP SEQUENCE FROM N.A.

RC STRAIN-CSTBL/61; TISSUE-Liver;

RX MEDILINE-21085660; PubMed-11217851;

RX MEDILINE-21085660; PubMed-11217851;

RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kando S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kando S., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Masuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kadota K., Okido T., Furuno M., Nano H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boill C., Fletcher C., Fujita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Auraki H., Toyo-oka K., Wang K.B., Weitz C., Whitaker C., Wilming L.,

RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPH2_MOUSE STANDARD; PRT; 617 AA.

Q9JIA7; Q9DBH6; Q9JVA9;

15-JUN-2002 (Rel. 41, Created)

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Sphingosine kinase 2 (EC 2.7.1.-) (SK 2) (SFK 2).
EMBL; AF245448; AAF74125.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thompson D., Pyne S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Milstier S., Kohama T., Spiegel S.;
"Molecular cloning and functional characterization of a novel mammalian sphingosine kinase type 2 isoform.";
J. Biol. Chem. 275:19513-19520(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20347850; PubMed=10751414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND CHARACTERIZATION STRAIN=ICR; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SPHINGOSINE KINASE FAMILY.
                                                                                                                                                                                                                                                                 dihydrosphingosine.
CATALYTIC ACTIVITY: Sphingosine + ATP • sphingosine 1-phosphate
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                                                             (See http://www.isb-sib.ch/announce/
                                                                                                    There are no restrictions ong as its content is in
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Murinae; Mus
                                                                                    and for
                                                                                                                                                       a collaboration
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RESULUT 3
SPH2_H
SPH2_H
SPH2_H
AC 09NRAO
DT 15-JUN
DT 15-JUN
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DT 15-JUN
DT SPHK2.
OS HOMO S
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Best I
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                                                                                                        15-JUN-2002
15-JUN-2002
                                                                                                                             SPH2_HUMAN STANDARD; PI
Q9NRAO; Q9NWU7; Q9HOQ2; Q9BRN1;
15-JUN-2002 (Rel. 41, Created)
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                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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EMBL;
SEQUENCE FROM N.A. MEDLINE-20347850; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom;
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                                          K2;
no sapiens (Human).
no sapiens (Human).
no sapiens (Human).
No sapiens (Human).
                                                                                                                                                                                                         Q 616
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                                                                                                                                                                                                                                                              ECPYLYYYPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMVSGCVEPPPSWKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MRFTLGTFLRLAALRTYRGRLAYLPV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLPRKPRLLILVNPFGGRGLAWQRCMDHVVPMISEAGLSFNLIQTERQNHARELVQGLSL
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AK004951; BAB23694.1;
BC006941; AAH06941.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192;
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510
548
617 /
                                                                                            (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
kinase 2 (EC 2.7.1.-) (SK 2) (SPK
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   . (ISOFORM 2), AN PubMed-10751414; ., Nava V.E., Eds
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                                                     Craniata; Vertebrata;
Catarrhini; Hominidae,
                                                                                                                                                    PRT;
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-> T (IN REF. 1).
-> F (IN REF. 1).
40EE2C2C288BE26A CRC64;
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                      AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              892; DB 1;
No. 5.7e-70;
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 L.C.,
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                                                      Hominidae;
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Query Match
Best Local Similarity
                                           CONFLICT
SEQUENCE
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VARSPLIC
                                                                                                                                                                                                                                                                                       EMBL; AF245447; AAF74124.1;
EMBL; AL136701; CAB66636.1;
EMBL; BC006161; AAH06161.1;
EMBL; BC010671; AAH10671.1;
EMBL; AK000599; BAA91280.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the phosphorylation of sphingosine sphingosine 1-phosphate (SPP), a lipid mediator with be and extracellular functions. Also acts on D-erythro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watanabe K., Kumagai A., Itakura S., Y
Suzuki Y., Obayashi M., Nishi T., Shib
Nakamura Y., Isogai T., Sugano S.,
"NEDO human cDNA sequencing project.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Towards a catalog of human genes and proteins: sequencing analysis of 500 novel complete protein coding human cDNAs.' Genome Res. 11:422-435(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wiemann S., Weil B., Weilenreuther R., Gassenhuber
Ansorge W., Boecher M., Bloecker H., Bauersachs S.,
Lauber J., Duesterhoeft A., Beyer A., Koehrer K.,
Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe
                                                                                                                                                                                        SMART;
                                                                                                                                                                                                   ProDom;
                                                                                                                                                                                                                   Pfam; PF00781; DAGKc;
                                                                                                                                                                                                                              InterPro; IPR001206; DAGKc.
InterPro; IPR003622; DAG_kin_cat.
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                                                                                                                                                                                                                                                                                                                                                                             or send an
                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mammalian
                                                                                                                                                                        Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Carcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wambutt R., Korn B., Klein M., Poustka A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21154917;
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mammalian sphingosine kinase type 2 i
J. Biol. Chem. 275:19513-19520(2000).
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European Bioinformatics Institute. The
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          produced by alternative splicing.
SIMILARITY: BELONGS TO THE SPHINGOSINE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dihydrosphingosine, D-erythro-sphingosine and L-threo-
dihydrosphingosine.
CATALYTIC ACTIVITY: Sphingosine + ATP = sphingosine I-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown
                                                                                                                                                                                                                                                                          607092;
                                                                                                                                                                                     SM00046; DAGKC;
                                                                                                                                                                                                                                                             HGNC:18859; SPHK2
                                                                                                                                                                                                    PD005043; DAG_kin_cat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM
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                                       49
654
                                                                                                                                                                                                                                                                                                                                                                             equires a license agreement (See http://www.isb-sib.ch/announce, email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Lymph;
                                                                                                                                    Kinase; ATP-binding; Alternative splicing.

1 36 MISSING (IN ISOFORM 2 AND ISOFORM 3).

292 390 FERROLDLLINCSLILEGGGHPLDLLSVTLASGSRCESF
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                                           AA;
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                                          49
69217
44.0%;
39.8%;
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                                           MW;
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Score
Pred.
                                                                                                LSVAWGFVSDVDIOSERFRALGSARFTLGTVLGLATLHTYR
GRLSYLPATVEPASPTP -> PREDSDSSTSSSACPLWTTA
RSCPRAAASMPGSCPLLPQQLALGFSRFIQDRVNGGGGRIG
                                                         (IN ISOFORM 3).
P -> S (IN REF.
                                                                                     SLTCRGHTQRTLPAPAREGGGSLFLKNINVFICKKKKK
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                                           F73FFCEC930DA50F
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, Shibahara T., Tanaka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     characterization
2 isoform.";
886.5; DB 1
No. 1.9e-69;
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Bauersachs S., Blum I
Koehrer K., Strack I
er B., Tampe J., Heut
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                                                         2)
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               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
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STRAIN-168 / Marburg;

MEDILINE-95050642; PubMed-7961792;

Ahmed M., Borsch C.M., Taylor S.S., Vazquez-Laslop N., Neyfakh A.A.;

A protein that activates expression of a multidrug efflux transporter upon binding the transporter substrates.";

J. Biol. Chem. 269:28506-28513(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DMRU_BACSU STANDARD; PRT; 297 AA. P39074; 201-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                 "Systematic sequencing of the 283 kb 210 degrees-232 degrees the Bacillus subtilis genome containing the skin element and sporulation genes":
                                                                                                                                                                                                                                                                                MIZUNO M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97124195; PI
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
MEDLINE-98044033; PubMed-9384377;
                                                                                                                                            sporulation genes.";
Microbiology 142:3103-3111(1996)
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S..,
RA Borriss R., Bourster L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Bourster L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haisch J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobbayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Persecan E., Pulic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rambut K., Verilla B., Rapport G., Rey M., Reynolds S.,
RA Rapiro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Persecan E., Pulic P., Purnelle B., Rache M., Saddie Y.,
RA Ragger M., Ravolta C., Rocha E., Roche B., Roche M., Saddie Y.,
RA Rasardohi M., Tankoshi A., Tanaka T., Takahashi H., Takemaru K.,
RA Sekiguchi J., Sekowska A., Serror P., Shin B.S., Soldo B.,
RA Viarii A., Vamannoto H., Vamane K., Vasamoto K., Yata K.,
RA Viarii A., Vandenbu H., Vannier F., Vassumoto K., Yata K.,
RA Viarii A., Vandenbu H., Vannier F., Vassumoto K., Yata K.,
RA Viarii A., Vashikawa H.F., Zumstein E., Roshikawa H., Danchin A.;
RT Nature J. J., Schowska P.,
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EMBL: D844432; BAA12602.1; --
EMBL: 299116; CAB14331.1; --
SubtiList: BG10302; bmrU.
InterPro; IPR003218; Cons_bypoth)47.
InterPro; IPR003202; bAGKG.
InterPro; IPR003622; DAGKG.
InterPro; IPR003622; DAGKG.
Pfam: P00781; DAGKG; 1.
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TIGRFAMS; TIGR00147; 1.
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Nature 390:249-256(1997).
-i- SIMILARITY: TO E.COLI YEGS AND TO SYNECHOCYSTIS PCC 6803 SLL0036.
190 MRETLGTELRLAALRTYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHW 249 : |: :: :| :
                                                                                                             107 NLAKAAEALMAGKKTS-VDVCQMNDRYFLNFWG1-----GLIAETSNQ1NETEK-ALLGK 159
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PRODOM, PD010761;
SMART; SM00046; DAGKC; 1.
TIGREAMS; T1GR00160; MGSA; 1.
PROSITE; PS01335; METHYLGLYOXAL_SYNTH; 1.
PROSITE; PS01335; METHYLGLYOXAL_SYNTHASE.
Hypothetical protein; Complete proteome.
1 126
METHYLGLYOXAL SYNTHASE.
62
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Q55452;
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"Sequence analysis of the genome of the unicellular cys
Synechocystis sp. strain PCC6803. I. Sequence features
region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
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Pfam; PF02142; MGS; 1.
ProDom; PD005043; DAG_kin_cat; 1.
ProDom; PD010761; Methylgl_synth;
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Bacteria: Cyanobacteria; Chroccocca
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InterPro; IPR004363; Methylgl_synth.
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188
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                                                                                   19
                          70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: IN THE N-TERMINAL SECTION; METHYLGLYOXAL SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO B. SUBTILIS BMRU AND TO E. COLI YEGS.
GEGDSFIIASGGDGTVSGVAAALV-----NTGI--PLGIIPRGTANAFSVALGIPTQIPG
                          GRWDALVVMS-GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASL---NHYAG 125
                                                       LIFNPVAGQGNVERELDLIKEHLQSEI-NLKITFTSAEVNVTDQAKEIVKRIKQANEQSD 187
                                                                      -SIDRFTGELSYVQASRIEIETDTAKKA-DMDGEVYTHTPAVIQVLPQHIDML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGELMVSEAVQGQVHPNYFWMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISYF-----TSALRTV------SSAASFPMTLK---IDGEEI---
                                                                                                              40;
                                                                                                                                                                                                                                                                                                                                                                                                                               s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -KEEAVMLLVMNGQYIGTNRIPLPDASIEDGLLDVLICRN--TNLTALRELMSMEQG
                                                                                                                                                                                                                                                                                                                                                                       IPR001206; DAGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation updat
protein sil0036.
                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                         DAG_kin_cat.
MGS_like.
                                                                                                                           5.0%;
26.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chroococcales;
                                                                                                              26;
                                                                                                                           Score 100.5;
Pred. No. 0.3
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                                                                                                                                                                     BDB3D47B2990F6C5 CRC64;
                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433
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                                                                                                                                         DB 1;
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                                                                                                              23;
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                                                                                                           Gaps
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240
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RESULT
KDGI_HO
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EMBL; AF061936; AAC62010.1; -
EMBL; AF219903; AAF43006.1; -
EMBL; AF219908; AAF43006.1; -
EMBL; AF219908; AAF43006.1; -
EMBL; AF219909; AAF43006.1; -
EMBL; AF219910; AAF43006.1; -
EMBL; AF219910; AAF43006.1; -
EMBL; AF219912; AAF43006.1; -
EMBL; AF219913; AAF43006.1; -
EMBL; AF219914; AAF43006.1; -
EMBL; AF219915; AAF43006.1; -
EMBL; AF219915; AAF43006.1; -
EMBL; AF219916; AAF43006.1; -
EMBL; AF219917; AAF43006.1; -
EMBL; AF219919; AAF43006.1; -
EMBL; AF219919; AAF43006.1; -
EMBL; AF219920; AAF43006.1; -
EMBL; AF219921; AAF43006.1; -
EMBL; AF219923; AAF43006.1; -
EMBL; AF219924; AAF43006.1; -
EMBL; 
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075912; Q9WZ49;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Diacylglycerol kinase, iota (EC 2.7.1.107) (Diglyceride kinase) (DGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bowne S.J., Sullivan L.S., Ding L., Traer E., Prescott S.M., Birch D.G., Kennan A., Humphries P., Daiger S.P.; "Evaluation of human diacylglycerol kinase iota, DGKI, a homolog Drosophila rdgA, in inherited retinopathy mapping to 7q."; Mol. Vision 6:6-9(2000).

-i- CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol = ADP + 1,2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ding L., Traer E., McIntyre T.M., "The cloning and characterization kinase, DGK-iota.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entities requires a license agreement (See http://www.isb-sib.ch/ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diacylglycerol 3-phosphate.
-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
-!- SIMILARITY: BELONGS TO THE EUKARYOTIC DIACYLGLYCEROL KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 2 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 135-1065 FROM N.A., MEDLINE=20173854; PubMed=107068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99047655; PubMed-9830018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 YEQVTNEDLLTNCTLLLCRRLLSPMNLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10706894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iota).
     JOINED
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n diacylglycerol
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Best Local S
Matches 55
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Pfam; PP00609; DAGKa; 1.
Pfam; PP00781; DAGKa; 1.
PfoDom; PP005043; DAGKa; 1.
ProDom; PD005043; DAGKin_cat; 1
SMART; SM00248; ANK; 2.
SMART; SM00045; DAGKa; 1.
SMART; SM00045; DAGKa; 1.
SMART; SM00045; DAGKa; 1.
SMART; SM00045; DAGKa; 1.
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SEQUENCE
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PROSITE; PS50088; ANK_REP_REGION; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50297; ANK_REP_BIND_DOM_1; FALSE_NEG.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; FALSE_NEG.
Transferase; Kinase; ANK_REPEAT; Repeat; Nuclear protein;
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InterPro; IPR003622;
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EELEDGYCKLPLNYFNNYFSL--GFDAHVTLEFHESREANPEKF 554
                                                                        PLGTGNDLARTLNWGGGY---TDEPV----SKILCQVEDGTVVQLDRWNLHVERNPDLPP
                                                                                                     PAGSGNALAASLNHYAGYEQVTNEDLLTNCTLLLCR----RLLSPMNLLSLHTASG-----
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                                    -RQVFDLSQEGPKDALELYRKVPNLRILACGGDGTVGWILSILDE---LQLSPQPPVGVL 459
                                                                                                                                                                                                      ARELVRSEELGRWDAL------VVMSGDGLMHEVVNGLMERPDWETAIOKPLCSL 108
                                                                                                                                                                                                                                                  PISSP---LMKP--LLVFVNPKSGGNQGTKVLQMFMWYLNP--------
                                                                                                                                                                                                                                                                                         PAGGPRGVLPRPCRVLVLLNPRGGKG----KALQLFRSHVQPLLAEAEISFTLMLTERRNH 59
                                                                                                                                                                                                                                                                                                                                  Similarity 24.6
55; Conservative
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IPR000756; DAGKa.
IPR001206; DAGKC.
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DAG_kin_cat.
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CATALYTIC-B (POTENTIAL).
ANK 1.
ANK 2.
POLY-ALA.
POLY-SER.
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L -> F.
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A -> P (IN REF. 2).
W; B84971AA7630A799 CRC64;
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RESULT 8
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EMBL; AE003839; AAF59180.1;
EMBL; X67335; CAA47750.1; -
PIR; S25099; S25099
PIR; S25099; S28229
PIR; A46140; A46140.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD002939; DAGKa; 1.
ProDom; PD005043; DAG_kin_cat;
SMART; SM00045; DAGKa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00609; DAGKa; 1. Pfam; PF00781; DAGKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBqn0004568; Dgk.
InterPro; IPR001756; DAGKa.
InterPro; IPR001206; DAGKc.
InterPro; IPR003622; DAG_kin_cat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·<del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                               290
                                                                                                            174
                                                                                                                                           234
                                                                                                                                                                                                                                                                     131
                                                                                                                                                                        127
                                                                                                                                                                                                                                                                                                  15 CRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNH-----ARELVRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diacylglycerol 3-phosphate.

TISSUE SPECIFICITY: EXPRESSED IN THE MERVOUS SYSTEM AND MUSCLE.
DEVELOPMENTAL STAGE: DGK IS TRANSCRIBED IN THE EMBRYONIC, PUPAL
AND ADULT STAGES, WITH LITTLE EXPRESSION DURING THE LARVAL
STAGES. EXPRESSION IN LATE EMBRYOS IS SPECIFIC TO THE CENTRAL
NERVOUS SYSTEM AND HEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no waified and this statement is not removed. Usage by and for commercial contents of the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVITY (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + 1,2-diacylglycerol =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: UPON CELL STIMULATION CONVERTS THE SECOND MESSENGER DIACYLGLYCEROL INTO PHOSPHATIDATE, INITIATING THE RESYNTHESIS OF PHOSPHATIDYLINOSITOLS AND ATTENUATING PROTEIN KINASE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE EUKARYOTIC DIACYLGLYCEROL KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                            VVDKSL-MERFEEIQRQSKQVATSMGTAASST
                                                                                                            IADVDLESEKYRRLGEMRFTLGTFLRLAALRT
                                                                                                                                         EGENIPKLMDKFRRASTVMLDRWSIEVTNTPHSDDMRPKVTLHS----NMQKVIELSQSV
                                                                                                                                                                        EQVTNEDLLTN----CTLLLCRRLLSPMNL-----
                                                                                                                                                                                                    DLPRF-RVICCGGDG----TVGWVLEAMDSIELASQPAIGVIPLGTGNDLARCLRWGGGY
                                                                                                                                                                                                                                 ELGRWDALVVMSGDGLMHEVVNGLMERPD·WETAIQKPLCSLPAGSGNALAASLNHYAGY
                                                                                                                                                                                                                                                                  CPLLVEVNPKSGGRQGDRILR------KFQYMLNPRQVYDLSKGGPKEGLTLFK 178
                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00046;
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                             791 AA;
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinase.
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAGKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF59180.1;
                                                                                                                                                                                                                                                                                                                                                                                                                             372
405
453
539
256
755
374
                                                                                                                                                                                                                                                                                                                                                                                               87297
                                                                                                                                                                                                                                                                                                                                                4.6%;
23.1%;
                                                                                                                                                                                                                                                                                                                                                                                               MW.
                                                                                                                                                                                                                                                                                                                                                                                                        POLY-ALA.
GLN-RICH.
POLY-GLN.
CATALYTIC-A (POTENTIAL).
CATALYTIC-B (POTENTIAL).
M -> T (IN REF. 1).
0 -> 00000 (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .'
                                                                                                                                                                                                                                                                                                                                                Score 93.5;
Pred. No. 3
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                             9DFD00E280FD64A6 CRC64;
                                                                                                                                                                                                                                                                                                                                 Mismatches
   712
                                                                                                           205
                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                     -LSLHTASGLRLFSVLSLAWGF
                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP + 1,2-
                                                                                                                                                                                                                                                                                                                                                              791;
                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                  67
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Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P49421;
01-FEB-1996 (Rel. 3
01-FEB-1996 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                       DOMAIN
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thorbjarnardottir S.H., Jonsson Z.O., Andresson O.S., Kristjansson J.K., Eggertsson G., Palsdottir A.; Rristjansson J.K., Eggertsson G., Palsdottir A.; "Cloning and sequence analysis of the DNA ligase-encoding of Rhodothermus marinus, and overproduction, purification and characterization of two thermophilic DNA ligases.";
                                                                                                                                                                    ProDom: PD003944; DNALigas:
SMART; SM00292; BRCT; 1.
SMART; SM00478; ENDO3c; 1.
SMART; SM00478; HhH1; 3.
SMART; SM00532; LIGANC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . . . .
                                                                                                             TIGREAMS; TIGR00575; dnlj; 1.

PROSITE: PS50172; BRCT; 1.

PROSITE: PS01055; DNA_LIGASE_N1;

PROSITE: PS01056; DNA_LIGASE_N2;
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U10483; AAA93198.1; -. HSSP; O87703; 1B04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodothermus marinus (Rhodothermus obamensis)
Bacteria; Bacteroidetes; Sphingobacteria; Sph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA ligase (EC
                                                                                                                                                                                                                                            Pfam; PF03119; DNA_ligase_ZBD; 1.
Pfam; PF03120; DNA_ligase_OB; 1.
                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                      Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95369716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-R-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=29549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crenotrichaceae;
                                                                                                   Ligase;
                                                                                                                                                                                                                                                                                                                  InterPro; IPR004149; Znf_DNAligase_C4.
                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: NAD(+) + {deoxyribonucleotide}(N) + {deoxyribonucleotide}(M) - AMP + nicotinamide nucleotide + {deoxyribonucleotide}(N+M) - MISCELLANEOUS: THIS ENZYME IS THERMOSTABLE.
SIMILARITY: BELONGS TO THE NAD-DEDENDENT DNA LIGASE FAMILY.
SIMILARITY: CONTAINS 1 BRCT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e 161:1-6(1995).

FUNCTION: THIS PROTEIN CATALYZES THE FORMATION OF PHOSPHODIESTER LINKAGES BETWEEN 5'-PHOSPHORYL AND 3'-HYDROXYL GROUPS IN DOUBLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDED DNA USING NAD AS A COENZYME AND AS THE ENERGY SOURCE FO
THE REACTION. IT IS ESSENTIAL FOR DNA REPLICATION AND REPAIR OF
DAMAGED DNA. THIS ENZYME IS THERMOSTABLE BEING ACTIVE AT 5-75
DEGREES CELSIUS WITH APPARENT OPTIMAL ACTIVITY ABOVE 55 DEGREES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELSIUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                    PF00633; HHH; 1.
PF01653; DNA_ligase_N; 1.
                                                                                                                                                                                                                                                                                                      PF00533; BRCT;
                                                                                                   DNA repair;
                                                                                                                                                                                                                                                                                                                                              IPR003583; HHH_1.
                                                                                                                                                                                                                                                                                                                                  IPR000445; HhH.
                                                                                                                                                                                                                                                                                                                                                              IPR003265; Endo_3c
                                                                                                                                                                                                                                                                                                                                                                          IPR004150; DNA_ligase_OB
IPR001679; DNAligase.
                                                    153
712
                                                                                                                                                                                                                                                                                                                                                                                                      IPR001357; BRCT
                                                         ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.5.1.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodothermus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33, Created)
33, Last sequence update)
40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=7642120;
                                                                                                  DNA replication;
                                                         79487 MW;
              4.68;
21.88;
                                                                                                                                                                                                                              igase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Polydeoxyribonucleotide
              Score 93;
Pred. No.
                                                                       AMP
                                                                                    BRCT
                                                        MP (BY SIMILARITY).
893AD3A78F77FFC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions
              DВ
2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sphingobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as its content
                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
                          Length 712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthase [NAD+]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           γd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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Conservative

37;

Mismatches

Indels

80;

Gaps

11;

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InterPro; IPR001206; DAGKC.
InterPro; IPR003622; DAG_Kin_cat.
ProDom; PD055043; DAG_Kin_cat; 1.
SMART; SM00046; DAGKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U39850; AAA81060.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein F52C9.3 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WormPep; F52C9.3; CE29806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   624 TQRLPEEAPAAESPVRGKTFVLTGALPHLTRKEAEELIKRAGGRVASSV 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ---LEEPVPSHWTVVPDEDFVLVLALLH--SHLGSEMFAAPMGRCAAGV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 TTAELLVQRFASIDELAAATIDELAALEGVGPITAESIANWFRVEDNRRLIEELKELGVN 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 --NLLSLHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A
                                                                   DALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGN 114
                                                                                                                               RPKRVFVLVNVEGNSRGCFDQFNKNALPLFHLAGVQVDVVKADNQAQLEALAGAVDTQEA 125
                                                                                                                                                                                          RPCRVLVLLNPRGGKGKALQLFRSHVQPLLAEAEISFTLMLTERRNHARELVRSEELGRW 72
   DILYVVGGDGTIGTVVTGIFRNRE---KAQLPVGFYPGGYDN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLAYLPVGRVGSKTPASPVVVQQ------GPVDAHLVP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEDLLKLEGFAETRARNLLRA-----IEASKQRPLSRLLFGLG-----IRHVGK 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPAGSGNALAAS------LNHYAGYEQVTNEDLLTNCTLLLCRR-LLSPM----- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HNEDYVRSRDIRIGDLVVVIRAGDVIPQVVRPVVEARTGNERP-WRMPERCPSCGSQLVR 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HARELVRSEELGRWDALVVMSGDGLMHEVVNGLM-----ERPDWETAIQKPLCS----- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPGEADYYCVASDCPAQFVRLLEHFAGRDAMDIEGMGSQVARQLAESGLVRPLSDLYRLK 519
                                                                                                                                                                                                                                                                     1 Similarity
27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 al protein
439 AA;
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                             49974 MW; 779850DC696E2D8B CRC64;
                                                                                                                                                                                                                                                          4.6%; Score 92.5; DB 1; Length 439; 26.5%; Pred. No. 1.7; tive 14; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 AA
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GVD2_HALN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AECOS156; AAG20894.1; -. Gas vesicle; ATP-binding; Plasmid; Complete proteome. NP_BIND 39 46 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVPD protein 2.
GVPD2 OR VNG6240G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9ннт2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVD2_HALN1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pNRC200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Halobacterium sp. (strain NRC-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
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300 VL-----PAIRNFLANEMG------VAVVP-----PKEGSPGLLHNDLSA 333
                                                           286 HLFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGK-GVFAVDGEL 344
                                                                                                                           245 SVPDEATWEPLANPTARFSTGIRDLDTILSGGFNRGGVVHLDLG----ADLSRDAWSVL
                                                                                                                                                                                              231 QGPVDAHLVPLEEPVPSHWTVVPDEDFVLV-----LALLHSHLGSEMFAAPMGRCAAGVM 285
                                                                                                                                                                                                                                                              195 HVTDNERGRTRRQ------LRLEKLRGVRIENRLQPFTLADGQFKAITPVELSTTQ
                                                                                                                                                                                                                                                                                                                      177 --VDLESEKYRRLGEMRFTLGTFLRLAALRTYR--GRLA--YLPVGRVGSKTPASPVVVQ 230
                                                                                                                                                                                                                                                                                                                                                                                         154 IETVTNQ------LVALARDAGVRLVLVSETATQSPLEYIVDGVVTL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 YEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVLSLA-----WGFIAD----- 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 LLVNGAPGTGKTLFTIRG-LDVLSREGDVLYVSTRVDQETVYEMYVEGHAALDRTALLDL 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQDPFGLPMDVDVPFETLNLESLLSWVDAISAPATKLTLAFDSWRLVYEYLAARiiDSPPS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGD--GLMHEV-----VNGLMERPDWETAIQKPLCSLPAGSGN-----ALAASLNHYAG 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492 AA; 53928 MW;
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36; Mismatches 146; Indels 95;
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